

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:17 ; Search time 117 Seconds

(without alignments)
1637.343 Million cell updates/sec

Title: US-10-761-593a-18

Perfect score: 2323
Sequence: 1 MGVHECPAFLWLLSLSLP.....MHFALHNYTKSLSPGK 436

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2323	100.0	436	7 ADM33853	Adm33853 Human HuE
2	2323	100.0	436	8 ADR48984	Adr48984 HuEPO-L-P
3	2323	100.0	436	8 ADM47516	Adm47516 Human Ery
4	2323	100.0	436	9 AEA18933	Aea18933 Human ery
5	2323	100.0	436	9 AEA88753	Aea88753 Human ery
6	2216.5	95.4	435	7 ADM33857	Adm33857 Human HuE
7	2216.5	95.4	435	8 ADR48988	Adr48988 HuEPO-L-V
8	2216.5	95.4	435	8 ADM47520	Adm47520 Human EPO
9	2216.5	95.4	435	9 AEA18937	Aea18937 Human ery
10	2216.5	95.4	435	9 AEA88757	Aea88757 Human ery
11	2212.5	95.2	437	7 ADM33855	Adm33855 Human HuE
12	2212.5	95.2	437	8 ADR48986	Adr48986 HuEPO-L-V
13	2212.5	95.2	437	8 ADM47518	Adm47518 Human EPO
14	2212.5	95.2	437	9 AEA18935	Aea18935 Human ery
15	2212.5	95.2	437	9 AEA88755	Aea88755 Human ery
16	2168.5	93.3	441	9 AEB70229	Aeb70229 EPO analo
17	2108	90.7	428	8 ABU64200	Abu64200 Plasmid P
18	2108	90.7	428	8 ADO10513	Ado10513 EPO signa
19	2108	90.7	428	8 ADV97050	Adv97050 Human Ery
20	2058	88.6	420	5 AAE15348	Aae15348 Human ery
21	1958.5	84.3	425	7 ABU64199	Abu64199 Plasmid P
22	1958.5	84.3	425	8 ADO10511	Ado10511 Kb signal
23	1929	83.0	444	9 ADV97042	Adv97042 Human EPO
24	1348.5	58.0	448	7 ADM33376	Adm33376 Human GCS

25	1348.5	58.0	448	9 ADV91791	Adv91791 Human GCS
26	1348.5	58.0	448	9 ADV99712	Adv99712 hg-CSF-L-
27	1347	58.0	432	8 ADM50823	Adm50823 Human int
28	1264.5	54.4	408	8 ADO95471	Ado95471 Fusion pr
29	1264.5	54.4	408	8 ADO95473	Ado95473 Fusion pr
30	1264.5	53.5	469	9 AEA5895	Aea5895 Human mon
31	1242	53.5	447	7 ADM33380	Adm33380 Human GCS
32	1242	53.5	447	7 ADM33380	Adm33380 Human GCS
33	1242	53.5	447	7 ADM33380	Adm33380 Human GCS
34	1240.5	53.4	431	8 ADM50827	Adm50827 Human int
35	1239	53.3	450	2 AAW34505	Aaw34505 Heavy cha
36	1239	53.3	450	2 AAY08755	Aay08755 Human IgG
37	1239	53.3	450	5 ABG31890	Abg31890 Full leng
38	1239	53.3	450	8 ADM18343	Adm18343 Antno ac1
39	1238	53.3	326	8 ADP77155	Adp77155 Anti-VAP-
40	1238	53.3	387	8 ADU66957	Adu66957 Murine pr
41	1238	53.3	409	8 ADQ95440	Adq95440 Fusion pr
42	1238	53.3	409	8 ADQ95441	Adq95441 Fusion pr
43	1238	53.3	447	8 ADQ17121	Adq17121 Humanised
44	1238	53.3	449	7 ADM33378	Adm33378 Human GCS
45	1238	53.3	449	9 ADV91793	Adv91793 Human GCS

ALIGNMENTS

RESULT 1	ADM33853	standard; protein; 436 AA.
ID	ADM33853	standard; protein; 436 AA.
XX	ADM33853;	
AC	ADM33853;	
XX		
DT	03-JUN-2004	(first entry)
XX		
DE	Human HuEPO-L-vFcgamma2 fusion protein.	
XX		
KW	Erythropoietin; EPO; immunoglobulin; IgG;	
KW	fragment crystallisation region; Fc; chronic anaemia; renal disease;	
KW	cancer chemotherapy; rheumatoid arthritis; AIDS;	
KW	myelodysplastic syndrome; (HuEPO)-L-vFcgamma2; human.	
OS	Homo sapiens.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..27
FT	Protein	/note= "Signal peptide"
FT		28..192
FT		/note= "EPO"
FT	Peptide	193..208
FT	Protein	/note= "Linker"
FT		209..436
FT		/note= "IgG2 Fc"
FT	Misc-difference	390
FT		/note= "Wild-type Pro substituted by Ser"
XX		
PN	US2003082749-A1.	
XX		
PD	01-MAY-2003.	
XX		
PF	17-AUG-2001; 2001US-00932812.	
XX		
PR	17-AUG-2001; 2001US-00932812.	
XX		
PA	(SUNT/) SUN L K.	
PA	(SUNT/) SUN B N C.	
PA	(SUNT/) SUN C R Y.	
XX		
PI	Sun LK, Sun BNC, Sun CRV;	
XX		
DR	WPI; 2003-616080/58.	
XX		

New recombinant human erythropoietin-L-vFc fusion proteins, useful for

PT treating patients with chronic anemia caused by renal failure, cancer
PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
PT infection.

XX Claim 3; Fig 2A; 14pp; English.

XX The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
XX fusion protein comprising HuEPO, a peptide linker, and a human
XX immunoglobulin G Fc (fragment crystallisation region) variant. Also
XX included is a carbohydrate-derived cell line producing the human
XX erythropoietin-L-vFc fusion protein cited above in its growth medium in
XX excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
XX -L-vFc fusion protein exhibits an enhanced in vitro biological activity
XX of at least 2-fold relative to that of recombinant HuEPO on a molar
XX basis. The flexible peptide linker containing about 20 or fewer amino
XX acids is present between HuEPO and the human IgG Fc variant. The IgG Fc
XX contains amino acid mutations to attenuate effector functions. The human
XX IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
XX Pro31Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
XX human IgG1 with Leu234Val, Leu235Ala and Pro31Ser mutations. The
XX recombinant human erythropoietin-L-vFc fusion proteins are useful for
XX treating patients with chronic anaemia caused by renal failure, cancer
XX chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
XX infection, or myelodysplastic syndrome. The increased activity and
XX prolonged presence of the human erythropoietin-L-vFc fusion protein in
XX the serum, as compared to prior art, leads to lower dosages and less
XX frequent injections. Less fluctuations of the drug in serum
XX concentrations means improved safety and tolerability, and less frequent
XX injections result in better patient compliance and quality of life. The
XX present sequence represents the fusion protein HuEPO-L-vFcgamma2.

XX Sequence 436 AA;

XX Query Match 100.0%; Score 2323; DB 7; Length 436;
XX Best Local Similarity 100.0%; Pred. No 6, 3e-155;
XX Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVECPAMWMLLSLISLPGLPVGAPPRILCDNRVTERLYLLENKENTTTGCAENC 60
DB 1 MGVECPAMWMLLSLISLPGLPVGAPPRILCDNRVTERLYLLENKENTTTGCAENC 60
QY 61 SINENITVPTDKVNFYAMKMEVGQAIVEVQGLLSEAVLRGALLVNSSQPMPELDL 120
DB 61 SINENITVPTDKVNFYAMKMEVGQAIVEVQGLLSEAVLRGALLVNSSQPMPELDL 120
QY 121 HYDKAVSGRLSTLTLLRALGAQKEAISPPDAASAPLRITTTADTFERKLPFRVSNPLRGKL 180
DB 121 HYDKAVSGRLSTLTLLRALGAQKEAISPPDAASAPLRITTTADTFERKLPFRVSNPLRGKL 180
QY 181 KYTGGACRTGDSGGSGGGSGGGSEKRCVCEPCPAPVAPSPVFLFPKPKDYL 240
DB 181 KYTGGACRTGDSGGSGGGSGGGSEKRCVCEPCPAPVAPSPVFLFPKPKDYL 240
QY 181 KYTGGACRTGDSGGSGGGSGGGSEKRCVCEPCPAPVAPSPVFLFPKPKDYL 240
DB 181 KYTGGACRTGDSGGSGGGSGGGSEKRCVCEPCPAPVAPSPVFLFPKPKDYL 240
QY 241 MISRTPEVTCVVVDVSHEDPEVFNNYVDGEVHNKTKREBQFSTFEVSVLTIVVQ 300
DB 241 MISRTPEVTCVVVDVSHEDPEVFNNYVDGEVHNKTKREBQFSTFEVSVLTIVVQ 300
QY 301 DMNGEYKCKVKNKGLPASIEKTIKTKGQPREPOVYTLPPREEMTKNQVSLTCLVKG 360
DB 301 DMNGEYKCKVKNKGLPASIEKTIKTKGQPREPOVYTLPPREEMTKNQVSLTCLVKG 360
QY 361 FYPSDIAVWESWGQENNYKTPPMLDPSGFYVSKLVDSRRKQGGVFCVWNNHA 420
DB 361 FYPSDIAVWESWGQENNYKTPPMLDPSGFYVSKLVDSRRKQGGVFCVWNNHA 420
QY 421 LNNHYTKSLISLSPGK 436
DB 421 LNNHYTKSLISLSPGK 436

RESULT 2
ADR48984
ID ADR48984 standard; protein; 436 AA.

XX ADR48984;
XX 02-DEC-2004 (first entry)
XX HuEPO-L-Fc fusion protein.
XX anti-anemic; nephrotoxic; human; HuEPO-L-vFc; erythropoietin; EPO;
XX anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
XX AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
XX Homo sapiens.
XX Synthetic.
XX US2004175824-A1.
XX 09-SEP-2004.
XX 21-JAN-2004; 2004US-00761593.
XX 17-AUG-2001; 2001US-00932812.
XX (SUNL/) SUN L K.
XX (SUNB/) SUN B N C.
XX (SUNC/) SUN C R Y.
XX Sun LK, Sun BNC, Sun CRY;
XX WPI; 2004-634851/61.
XX N-PSDB; ADR48983.
XX New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
XX (HuEPO), a peptide linker, and a human IgG Fc variant, useful for
XX treating chronic anemia due to renal diseases, cancer chemotherapy, or
XX rheumatoid arthritis.
XX Claim 3; SEQ ID NO 18; 31pp; English.
XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
XX (HuEPO), a peptide linker, and a human IgG Fc variant, is new.
XX INDEPENDENT CLAIMS are also included for the following: a chinese hamster
XX ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in
XX its growth medium in excess of 10 microg/g per million cells in a 24 hour
XX period; and a method for making a recombinant fusion protein comprising
XX HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred
XX protein: The peptide linker containing 20 or fewer amino acids is present
XX between HuEPO and the human IgG Fc variant, and comprises two or more
XX amino acids selected from glycine, serine, alanine, and threonine. The
XX human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human
XX IgG2 with Pro31Ser mutation comprising 436 amino acids (SEQ ID NO. 18).
XX It also comprises a hinge, CH2, and CH3 domains of human IgG4 with
XX Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.
XX 20). It further comprises a hinge, CH2, and CH3 domains of human IgG1
XX with Leu234Val, Leu235Ala, and Pro31Ser mutations comprising 435 amino
XX acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro
XX biological activity similar to or higher than that of rHuEPO on a molar
XX basis. Preferred CHO-derived cell line: The CHO-derived cell line
XX producing the HuEPO-L-vFc fusion protein in its growth medium in excess
XX of 30 microg/g per million cells in a 24 hour period. The human IgG Fc
XX variant comprises a hinge, CH2, CH3 domains of human IgG selected from
XX IgG1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,
XX the IgG Fc contains amino acid mutations to attenuate effector functions,
XX a flexible peptide linker containing 20 or fewer amino acids is present
XX between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion
XX protein exhibits in vitro biological activity similar to or higher than
XX that of rHuEPO on a molar basis. Preferred Method: Making a recombinant
XX fusion protein comprising HuEPO, a flexible peptide linker, and a human
XX IgG Fc variant comprising generating a CHO-derived cell line; growing the
XX cell line where the recombinant protein is expressed in its growth medium
XX in excess of 10 microg/g per million cells in a 24 hour period; and
XX purifying the expressed protein from (b) where the recombinant fusion
XX protein exhibits in vitro biological activity similar to or higher than
XX that of rHuEPO on a molar basis. Anti-anemic; Nephrotoxic. No biological

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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:21 ; Search time 21.333 Seconds
(Without alignments)
1966.430 Million cell updates/sec

Title: US-10-761-593A-18

Perfect score: 2323

Sequence: 1 MGWHECPRAWMLLSLSLP.....MHEALNNHYTKSLSPGK 436

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1236	53.2	326	1 G2HU	Ig gamma-2 chain C
2	1148.5	49.4	374	2 S69339	Ig heavy chain V r
3	1138	49.0	255	4 S31866	Ig gamma-1 chain C
4	1137	48.9	330	1 G4HU	Ig gamma-1 chain C
5	1120.5	48.2	327	1 G4HU	Ig gamma-4 chain C
6	1120	48.2	377	2 A23511	Ig gamma-3 chain C
7	1111	47.8	377	2 A60764	Ig gamma-3 chain C
8	1102	47.4	289	1 G3H0W1	Ig gamma-3 heavy C
9	1088	46.8	234	2 PT0207	Ig gamma chain C r
10	994	42.8	328	2 ZUHU	erythropoietin pre
11	907	39.0	328	2 I47160	Ig gamma 2b chain
12	907	39.0	328	2 I47159	Ig gamma 2a chain
13	902.5	38.9	192	1 J00173	erythropoietin pre
14	900	38.7	272	2 I47162	Ig gamma 4 chain C
15	897.5	38.6	192	2 I84613	erythropoietin pre
16	887	38.2	328	2 I47158	Ig gamma 1 chain C
17	885	38.1	328	2 I47161	Ig gamma 3 chain C
18	872.5	37.6	323	1 GHRB	Ig gamma chain C r
19	858.5	37.0	329	1 G2GP	Ig gamma-2 chain C
20	854	36.8	470	2 S22080	Ig heavy chain pre
21	833	35.9	444	2 PC4436	monoclonal antibody
22	832.5	35.8	308	2 C30554	Ig heavy chain C r
23	832.5	35.8	472	2 S31459	Ig gamma-1 chain C
24	832	35.8	326	2 B80017	Ig gamma-1 chain C
25	823	35.4	324	1 G1MS	Ig gamma-1 chain C
26	818	35.2	329	1 G1MSC	Ig gamma-3 chain C
27	809.5	34.8	333	2 G1MSM	Ig gamma-1 chain C
28	809.5	34.8	333	2 PS0018	Ig gamma-2b chain
29	807	34.7	398	1 G3MSM	Ig gamma-3 chain C

30	805.5	34.7	329	2 S00847	Ig gamma-2c chain
31	797.5	34.3	188	1 I46083	erythropoietin pre
32	794	34.2	322	2 PS0019	Ig gamma-2a chain
33	788.5	33.9	469	2 S37483	Ig gamma-2a chain
34	786	33.8	327	2 S06611	Ig gamma-2 chain C
35	780.5	33.6	330	1 G2MSA	Ig gamma-2a chain
36	775.5	33.4	399	1 G2MSAM	Ig gamma-2a chain
37	771.5	33.2	192	1 S28148	erythropoietin pre
38	768	33.1	474	1 G2MS11	Ig gamma-2b chain
39	767.5	33.0	335	1 G2MSAB	Ig gamma-2b chain
40	765.5	33.0	194	1 I46401	erythropoietin pre
41	765.5	33.0	446	2 S40295	Ig gamma-2a chain
42	761.5	32.8	190	2 I46578	erythropoietin - p
43	755.5	32.5	405	1 G2MSBM	Ig gamma-2b chain
44	751.5	32.4	192	1 A24902	erythropoietin pre
45	739.5	31.8	475	2 S01321	Ig gamma-2b chain

ALIGNMENTS

RESULT 1

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #ext_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co-
A:Reference number: A93906; PMID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1326 <EQL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:93
A>Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A:Reference number: A92809; PMID:81007873; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>
A:Cross-references: UNIPARC:UPI0000173791
A>Note: Trp-156 is at or near the complement-binding site
R:Connell, G.B.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; PMID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A>Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A:Reference number: A93132; PMID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOR>
A:Cross-references: UNIPARC:UPI0000173794
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ed
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstien, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1A C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F:2085/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:233-306/Domain: immunoglobulin homology <IM3>
F:1/Disulfide bonds: Interchain (co light chain) #status experimental
F:21-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: Interchain (co heavy chain) #status experimental
F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.2%; Score 1236; DB 1; Length 326;
Best Local Similarity 99.6%; Pred. No. 3.4e-77;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 209 ERKCCVCEPCPPAPVAGSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVQFWY 268
DB 99 ERKCCVCEPCPPAPVAGSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVQFWY 158
QY 269 DGEVHNAAKTKPREEQNSTFRVSVLTIVHODMNGEKYCKVSNKGLPASIEKTSKT 328
DB 159 DGEVHNAAKTKPREEQNSTFRVSVLTIVHODMNGEKYCKVSNKGLPASIEKTSKT 218
QY 329 KQGPREFQVYTLPPSRREMTKNQVSLTCLVKGFPSPDIABWESNGQPENNYKTPPMLD 388
DB 219 KQGPREFQVYTLPPSRREMTKNQVSLTCLVKGFPSPDIABWESNGQPENNYKTPPMLD 278
QY 389 SDGSGFFLYSKLTVDKSRWQGNVFCSVVMEALHNHYTKSLSPGK 436
DB 279 SDGSGFFLYSKLTVDKSRWQGNVFCSVVMEALHNHYTKSLSPGK 326

RESULT 2

S69339
Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R:Khamlich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-140 'C' 142-374 <KH2>
A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 49.4%; Score 1148.5; DB 2; Length 374;
Best Local Similarity 86.2%; Pred. No. 3.8e-71;
Matches 219; Conservative 8; Mismatches 18; Indels 9; Gaps 3;

QY 192 DSGGGGGGGGGGGG-----GSEKRCVVE---CPPCPAP-VAGPSVFLFPPPKKDTLM 242
DB 121 EGTGGQYRPHSGGGGGLTVVSSEPKSCDTHTCPPAPBELLGGGSVFLFPPPKKDTLM 180
QY 243 SRTPEVTCVVDVSHEDPEVQFNWYDGEVHNAAKTKPREEQNSTFRVSVLTIVHODM 302
DB 181 SRTPEVTCVVDVSHEDPEVQFNWYDGEVHNAAKTKPREEQNSTFRVSVLTIVHODM 240
QY 303 LNKKEYCKVSNKGLPASIEKTSKTQGPREFQVYTLPPSRREMTKNQVSLTCLVKGFPY 362
DB 241 LNKKEYCKVSNKGLPASIEKTSKTQGPREFQVYTLPPSRREMTKNQVSLTCLVKGFPY 300
QY 363 PSDIABWESNGQPENNYKTPPMLDSDGFFLYSKLTVDKSRWQGNVFCSVMEALH 422
DB 301 PSDIABWESNGQPENNYKTPPMLDSDGFFLYSKLTVDKSRWQGNVFCSVMEALH 360
QY 423 NHYTKSLSPGK 436
DB 361 NHYTKSLSPGK 374

RESULT 3

S31866
Ig gamma-1 chain C region - synthetic

C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filip, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FIL>
A:Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PIR
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 49.0%; Score 1138; DB 4; Length 255;
Best Local Similarity 90.9%; Pred. No. 1.3e-70;
Matches 211; Conservative 9; Mismatches 8; Indels 4; Gaps 2;

QY 209 ERKCCVCEPCPPAP-VAGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVQ 264
DB 24 ESKSCDKHTICPCPPAPBELLGGGSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVQ 83
QY 265 NWYVDGEVHNAAKTKPREEQNSTFRVSVLTIVHODMNGEKYCKVSNKGLPASIEKT 324
DB 84 NWYVDGEVHNAAKTKPREEQNSTFRVSVLTIVHODMNGEKYCKVSNKGLPASIEKT 143
QY 325 ISKTQGPREFQVYTLPPSRREMTKNQVSLTCLVKGFPSPDIABWESNGQPENNYKTP 384
DB 144 ISKTQGPREFQVYTLPPSRREMTKNQVSLTCLVKGFPSPDIABWESNGQPENNYKTP 203
QY 385 PMLDSDGFFLYSKLTVDKSRWQGNVFCSVVMEALHNHYTKSLSPGK 436
DB 204 PMLDSDGFFLYSKLTVDKSRWQGNVFCSVVMEALHNHYTKSLSPGK 255

RESULT 4

GHHU
Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S31887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Beysen, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:16 ; Search time 194.667 Seconds

(without alignments)
1580.190 Million cell updates/sec

Title: US-10-761-593A-18

Perfect score: 2323

Sequence: 1 MVEHCECPAMMLLSTLSTLP.....MHEALNHVYQKSLSPGK 436

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Uniprot 05.80.*
2: uniprot_sprot.*
3: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1236	53.2	326	1 IGHG2_HUMAN	P01859 homo sapien
2	1236	53.2	417	2 OGN093_HUMAN	O6N093 homo sapien
3	1233	53.1	464	2 OGMZU6_HUMAN	O6MZU6 homo sapien
4	1231	53.0	465	2 OGP6C4_HUMAN	O6P6C4 homo sapien
5	1222	52.6	470	2 O68CNA_HUMAN	O68CNA homo sapien
6	1146.5	49.4	487	2 O65ZL2_MUR1	O65ZL2 mus sp. fv/
7	1144	49.2	679	2 O96PQ8_HUMAN	O96PQ8 homo sapien
8	1143	49.2	348	2 O6PYX1_HUMAN	O6PYX1 homo sapien
9	1143	49.2	473	2 O6MZV7_HUMAN	O6MZV7 homo sapien
10	1143	49.2	478	2 O6P181_HUMAN	O6P181 homo sapien
11	1143	49.2	480	2 O6PJF1_HUMAN	O6PJF1 homo sapien
12	1137	48.9	330	1 IGHG1_HUMAN	P01857 homo sapien
13	1137	48.9	465	2 O6GMK6_HUMAN	O6GMK6 homo sapien
14	1137	48.9	466	2 O6IN78_HUMAN	O6IN78 homo sapien
15	1137	48.9	469	2 O659F4_HUMAN	O659F4 homo sapien
16	1137	48.9	469	2 O727P5_HUMAN	O727P5 homo sapien
17	1137	48.9	470	2 O725W1_HUMAN	O725W1 homo sapien
18	1137	48.9	470	2 O6PJU4_HUMAN	O6PJU4 homo sapien
19	1137	48.9	472	2 O6N089_HUMAN	O6N089 homo sapien
20	1137	48.9	475	2 O6SEF5_HUMAN	O6SEF5 homo sapien
21	1137	48.9	475	2 O6GMW7_HUMAN	O6GMW7 homo sapien
22	1137	48.9	476	2 O6GMK1_HUMAN	O6GMK1 homo sapien
23	1133	48.8	473	2 O6P055_HUMAN	O6P055 homo sapien
24	1133	48.8	475	2 O6MZQ6_HUMAN	O6MZQ6 homo sapien
25	1133	48.8	480	2 O6N094_HUMAN	O6N094 homo sapien
26	1133	48.8	481	2 O6N097_HUMAN	O6N097 homo sapien
27	1133	48.8	482	2 O72351_HUMAN	O72351 homo sapien
28	1130	48.6	466	2 O6N096_HUMAN	O6N096 homo sapien
29	1126.5	48.5	476	2 O6MZK7_HUMAN	O6MZK7 homo sapien
30	1126	48.5	475	2 O6N095_HUMAN	O6N095 homo sapien
31	1126	48.5	544	2 O6PJ95_HUMAN	O6PJ95 homo sapien

32	1123	48.3	521	2 O8N4Y9_HUMAN	O8N4Y9 homo sapien
33	1120.5	48.2	437	1 IGHG4_HUMAN	P01861 homo sapien
34	1120.5	48.2	473	2 O8TC63_HUMAN	O8TC63 homo sapien
35	1120	48.2	354	2 O86T72_HUMAN	O86T72 homo sapien
36	1120	48.2	518	2 O6N030_HUMAN	O6N030 homo sapien
37	1120	48.2	519	2 O5EBM2_HUMAN	O5EBM2 homo sapien
38	1117	48.1	475	2 O5R1E7_PONY	O5R1E7 pongo pygma
39	1112	47.9	509	2 O8NFI7_HUMAN	O8NFI7 homo sapien
40	1107	47.7	290	1 IGHG3_HUMAN	P01860 homo sapien
41	994	42.8	193	1 EPO_HUMAN	O549U2 homo sapien
42	994	42.8	193	2 O545U2_HUMAN	O549U2 homo sapien
43	902.5	38.9	192	1 EPO_MACRA	P07665 macaca fasc
44	897.5	38.6	192	1 EPO_MACMU	O28513 macaca mula
45	872.5	37.6	323	1 GC_FABIT	P01870 oryctolagus

ALIGNMENTS

RESULT 1
ID IGHG2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG gamma-2 chain C region.
GN Name=IGHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE OF 2-326.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma heavy
RT chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1986(1982).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 88-115.
RC TISSUE=Petal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP PROTEIN SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=674012;
RA Wang A.-C., Tung E., Pudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
RT evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP PROTEIN SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
RT domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP PROTEIN SEQUENCE OF 238-275 (ZIE).

RX MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;
 RA Hofmann T., Parr D.M.;
 RT A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN (7)
 RP SEQUENCE REVISION TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN (8)
 RP PROTEIN SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95265298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN (9)
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN (10)
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC -----
 DR EMBL J00230; AAB59393.1; -, Genomic_DNA.
 DR PIR; A93906; G2HU.
 DR HSSP; P01859; 1-326.
 DR SMR; P01859; 1-326.
 DR HGNC; HGNC:5526; IGHG2.
 DR MIM; 147110; -.
 DR GO; GO:0003624; C:membrane fraction; NAS.
 DR GO; GO:0003623; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-CL.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00407; IgC1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Direct protein sequencing; Immunoglobulin C region;
 KW Immunoglobulin domain.
 FT REGION 1 98
 FT REGION 99 110
 FT REGION 111 219
 FT REGION 220 326
 FT SITE 156 156
 FT DISULFID 14 14
 FT DISULFID 27 83
 FT DISULFID 102 102
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 FT DISULFID 106 106
 FT DISULFID 109 109
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT VARIANT 60 60
 FT NON TER 1
 FT CONFLICT 109 109
 FT NON TER 1
 SQ SEQUENCE 326 AA; 35885 MW; 83108786878CF9C CRC64;
 Query Match 53.2%; Score 1236; DB 1; Length 326;

Best Local Similarity 99.6%; Pred. No. 5.5e-84;
 Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 209 ERKCCVCEPCPCAPPAGPSVFLFPKPKDITLMIISTPVCVVVDVSHEDPEQFNWYV 268
 DB 99 ERKCCVCEPCPCAPPAGPSVFLFPKPKDITLMIISTPVCVVVDVSHEDPEQFNWYV 158
 QY 269 DGEVFNNAKTREBEQFNSTFRVSVLTIVHODMLNGKCYKCKVSKGAPASTIKTISK 328
 DB 159 DGEVFNNAKTREBEQFNSTFRVSVLTIVHODMLNGKCYKCKVSKGAPASTIKTISK 218
 QY 329 KGQPREPOVYTLPPSHEMTKNQVSLTCLVKGPYPSDIAVEMESNCPENNYKTPPMD 388
 DB 219 KGQPREPOVYTLPPSHEMTKNQVSLTCLVKGPYPSDIAVEMESNCPENNYKTPPMD 278
 QY 389 SDGSFPLYSKLTIVDKSRMOQGVFSCSVMEALAHNYTKSLSLSPGK 436
 DB 279 SDGSFPLYSKLTIVDKSRMOQGVFSCSVMEALAHNYTKSLSLSPGK 326
 RESULT 2
 ID 06N093 HUMAN PRELIMINARY; PRT; 417 AA.
 AC 06N093;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686i04196 (Fragment).
 GN Name=DKFZp686i04196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human esophagus tumor;
 RG The German Human CDNA Consortium;
 RA Wamburt R., Haubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fodor G., Han M., Wiemann S., Schmitt R.,
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640623; CAE4577.1; -, mRNA.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-CL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG-V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IgC1; 3.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 417 AA; 46061 MW; C4518B844CFB883C CRC64;
 Query Match 53.2%; Score 1236; DB 2; Length 417;
 Best Local Similarity 99.6%; Pred. No. 7.6e-84;
 Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 209 ERKCCVCEPCPCAPPAGPSVFLFPKPKDITLMIISTPVCVVVDVSHEDPEQFNWYV 268
 DB 190 ERKCCVCEPCPCAPPAGPSVFLFPKPKDITLMIISTPVCVVVDVSHEDPEQFNWYV 249
 QY 269 DGEVFNNAKTREBEQFNSTFRVSVLTIVHODMLNGKCYKCKVSKGAPASTIKTISK 328
 DB 250 DGEVFNNAKTREBEQFNSTFRVSVLTIVHODMLNGKCYKCKVSKGAPASTIKTISK 309
 QY 329 KGQPREPOVYTLPPSHEMTKNQVSLTCLVKGPYPSDIAVEMESNCPENNYKTPPMD 388
 DB 310 KGQPREPOVYTLPPSHEMTKNQVSLTCLVKGPYPSDIAVEMESNCPENNYKTPPMD 369

Page 2

Db 419 ALHNHYTKSLISPGK 435

RESULT 3
US-09-932-812A-20
Sequence 20, Application US/09932812A
Patent No. 6900292
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
APPLICANT: Sun, Hsiang-Yun
Title: A method for the detection of human retrovirus in with

```

/ TITLE OF INVENTION: activities
/ FILE REFERENCE: 02SDN2001
/ CURRENT APPLICATION NUMBER: US/09/932,812A
/ CURRENT FILING DATE: 2001-08-17
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 20
/ LENGTH: 437
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HuPO-1-vFc gamma4 with a 27-amino acid leader peptide
/ OTHER INFORMATION: (Figure 2B
/ OTHER INFORMATION: )
/ US-09-932-812A-20

Query March
Best Local Similarity 95.9%; Score 22.5; DB 2; Length 437;
Matches 419; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 MGVEHCAGWMLLSLISLPLGIPVIGAPRLICDSRYVERRYLLEAEENITTCAEHC 60
DB 1 MGVEHCAGWMLLSLISLPLGIPVIGAPRLICDSRYVERRYLLEAEENITTCAEHC 60
QY 61 SLNENITVPPTKCNFYAKMEVGOCAVEYWGIALISEVNLGQALLVNSSQWPEIQL 120
DB 61 SLNENITVPPTKCNFYAKMEVGOCAVEYWGIALISEVNLGQALLVNSSQWPEIQL 120
QY 121 HYDKAVSGILSLTLLRLALGAOKRAISPPDAASAPLRITTDTRFKLFRVYSNFIKGL 180
DB 121 HYDKAVSGILSLTLLRLALGAOKRAISPPDAASAPLRITTDTRFKLFRVYSNFIKGL 180
QY 181 KLYTGEACRTGDSGGSGSGSGSGSGSERKCCVCPDAPVYA-GPSVFLPPPKRDT 239
DB 181 KLYTGEACRTGDSGGSGSGSGSGSGSERKCCVCPDAPVYA-GPSVFLPPPKRDT 240
QY 240 LMIERTPEVTCVVVDVSHEDPEVOFNMYVDGVEVHNKAKTREREOFNSTFRVSVLTIVH 299
DB 240 LMIERTPEVTCVVVDVSHEDPEVOFNMYVDGVEVHNKAKTREREOFNSTFRVSVLTIVH 300
QY 300 QDMNLNGEYKCKVSNKGLPASIIEKTIKTKGQPREPQVYTLPPSRREMTKNQVSLTCLVK 359
DB 301 QDMNLNGEYKCKVSNKGLPASIIEKTIKTKGQPREPQVYTLPPSRREMTKNQVSLTCLVK 360
QY 360 GFYPSDIAVWESNGLPGQENNNYKTTTPPMLDSDGPFYLSKLTVDKSRMQOGNIFSCSWHE 419
DB 361 GFYPSDIAVWESNGLPGQENNNYKTTTPPMLDSDGPFYLSKLTVDKSRMQOGNIFSCSWHE 420
QY 420 AIHHHTYOKSLISLSPGK 436
DB 421 AIHHHTYOKSLISLSPGK 437

RESULT 4
US-09-968-362A-18
/ Sequence 18, Application US/09968362A
/ Patent No. 6797493
/ GENERAL INFORMATION:
/ APPLICANT: Sun, Lee-Hwei K
/ APPLICANT: Sun, Bill

```


QY	I	MGVHECPAMIMLLLSLSTPLGIPVLGAPRRLICDSRLERYLLFAKAEENITGGCAEH	60
Db	1	MGVHECPAMIMLLLSLSTPLGIPVLGAPRRLICDSRLERYLLFAKAEENITGGCAEH	60
QY	61	SLNENITVPTKYNFAMKRMVEVGOAAVEWGGALLSEAVLRGALLVNSQWPEPQL	120
Db	61	SLNENITVPTKYNFAMKRMVEVGOAAVEWGGALLSEAVLRGALLVNSQWPEPQL	120
QY	121	HYDKAVSGLSRLTTLRLALGAQKEAISPDDAASAPLRTITADTFRKLFRYSNPLRGL	180
Db	121	HYDKAVSGLSRLTTLRLALGAQKEAISPDDAASAPLRTITADTFRKLFRYSNPLRGL	180
QY	181	KLYTGEACRTDGSGGSGGGSGGGSGGSGSERKCVBECPCAPPVAGSEVFLFPPKPKDTL	240
Db	181	KLYTGEACRTDGSGGSGGGSGGGSGGSGSERKCVBECPCAPPVAGSEVFLFPPKPKDTL	240
QY	241	MISRTBEVTCVVVDVSHEDPEVOFMWYVDGVEVHNAKTKPRBEQNSIFRVASLTIVHQ	300
Db	241	MISRTBEVTCVVVDVSHEDPEVOFMWYVDGVEVHNAKTKPRBEQNSIFRVASLTIVHQ	300
QY	301	DMINGKEVKKYKSNKGLPASIEKTLSTKSGQREPOVYTLPPSRBEEMKNQVSLTCLVKG	360
Db	301	DMINGKEVKKYKSNKGLPASIEKTLSTKSGQREPOVYTLPPSRBEEMKNQVSLTCLVKG	360

OY	361	FPSPSLIAVWMEWGGOENNRYKTTPEMLDSDGSEFLYSKLTVDKSRWQOQGVFSCSWHEA	420
Db	361	FPPSDIAVWMEWGGOENNRYKTTPEMLDSDGSEFLYSKLTVDKSRWQOQGVFSCSWHEA	420
OY	421	LHNHYTQKSLSLSPGK	436
Db	421	LHNHYTQKSLSLSPGK	436

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RESULT 2
US-10-761-593A-18
: Sequence 18, Application US/10761593A
: Publication No. US20040175824A1
: GENERAL INFORMATION:
: APPLICANT: Sun, Lee-Hwei K
: APPLICANT: Sun, Bill N
: TITLE OF INVENTION: Pe fusion proteins of human erythropoietin with high biological
: TITLE OF INVENTION: activities
: FILE REFERENCE: 0250N2001-A
: CURRENT APPLICATION NUMBER: US/10/761,593A
: CURRENT FILING DATE: 2004-01-21
: PRIOR APPLICATION NUMBER: 09/932812
: PRIOR FILING DATE: 2001-08-17
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 18
: LENGTH: 436
: TYPE: PR1
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: HuPEO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure
US-10-761-593A-18

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[illegible]

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RESULT 3
US-11-016-518A-18
/ Sequence 18, Application US/11016518A
/ Publication No. US20050124045A1
/ GENERAL INFORMATION:
/ APPLICANT: Sun, Lee-Hwei K
/ APPLICANT: Sun, Bill N
/ TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
/ TITLE OF INVENTION: biological activities
/ FILE REFERENCE: 02SUN2004D1
/ CURRENT APPLICATION NUMBER: US/11/016,518A
/ PRIOR FILING DATE: 2004-12-17
/ PRIOR FILING DATE: 2001-08-17
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 18
/ LENGTH: 436
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: 2A)
US-11-016-518A-18

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[illegible]

Tue Apr 18 11:54:44 2006

us-10-761-593a-18.rapbn

Page 2

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Qy	236	PKRTLMISRPPEATCVVNDVSHEDPEVQENYAVDVEVHNKTKTPREQPFSTRVSVL				295
Db	228	PKRTLMISRPPEATCVVNDVSHEDPEVQENYAVDVEVHNKTKTPREQINSTRVSVL				287
Qy	296	TVVHODMLNGEKYKCVSNKGLPASLEKTIISTKGCQPRBPQVYITLPPSREMTNQVSLT				355
Db	288	TVVHODMLNGEKYKCVSNKGLPASLEKTIISTKGCQPRBPQVYITLPPSREMTNQVSLT				347
Qy	356	CLVKGFPSPDIAVEMESNCPENNYYKTPPMLDSDGSFLLYSKLTVDKSRMQQGNVPSCS				415
Db	348	CLVKGFPSPDIAVEMESNCPENNYYKTPPVLDSGSEFLYSKLTVDKSRMQQGNVPSCS				407
Qy	416	VMEBALHNHYTKQSLSLSPGK				436
Db	408	VMEBALHNHYTKQSLSLSPGK				428

RESULT 2
 US-11-029-003-16
 ? Sequence 16, Application US/11029003
 ? Publication No. US20050260194A1
 ? GENERAL INFORMATION:
 ? APPLICANT: PETERS, ROBERT T.
 ? APPLICANT: MEZO, ADAM R.
 ? APPLICANT: RIVERA, DANIEL S.
 ? APPLICANT: BITONTEI, ALAN J.
 ? APPLICANT: STAYTELL, JAMES
 ? TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
 ? FILE REFERENCE: 08945.0007-01000
 ? CURRENT APPLICATION NUMBER: US/11/029,003
 ? PRIOR FILING DATE: 2005-01-05
 ? PRIOR APPLICATION NUMBER: 60/539,207
 ? PRIOR FILING DATE: 2004-01-26
 ? PRIOR APPLICATION NUMBER: 60/487,964
 ? PRIOR FILING DATE: 2003-07-17
 ? PRIOR APPLICATION NUMBER: 60/469,600
 ? PRIOR FILING DATE: 2003-05-06
 ? NUMBER OF SEQ ID NOS: 91
 ? SOFTWARE: PatentIn Ver. 3.2
 ? SEQ ID NO 16
 ? LENGTH: 444
 ? TYPE: PRT
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ? OTHER INFORMATION: Construct
 ? US-11-029-003-16

Query Match	83.0%	Score 1929	DB 7	Length 444
Best Local Similarity	82.4%	Pred. 1.1e-144		
Matches	379	Conservative	10	Mismatches 23
			Indels	48
			Gaps	4
QY	7	PAMILLLSLSTLPGLPY-LGAPPRLLCDSDVLERLYLLEAKAEKIIITTCGAHCSINEN	65	
Db	3	PCTLLILLIAAALAPOTRAGSRAPRLRLDSDRVLYGRYLLEAKAEKIIITTCGAHCSINEN	62	
QY	66	ITVPPTKKNFYAMKMEVGOQAAVEWOGIATALLSEALRGOALLVNSGQWPEPLQIHLVDA	125	
Db	63	ITVPPTKKNFYAMKMEVGOQAAVEWOGIATALLSEALRGOALLVNSGQWPEPLQIHLVDA	122	
QY	126	VSGRLSTLTLLRALGAKKEAISPPDAASAAPRTITADPFRKLFYRYSNFLRKLLYTG	185	
Db	123	VSGRLSTLTLLRALGAKKEAISPPDAASAAPRTITADPFRKLFYRYSNFLRKLLYTG	182	
QY	186	EACRTGDSGGG-----SGGGSGGGSGSERKCCVECP	217	
Db	183	EACRTGDSGGG-----SGGGSGGGSGSERKCCVECP	226	
QY	218	PCPAPP-VAGSPVFLFPKPKDTLMSRTPEYTCVVADVDSHEPVEVOFNMVYDGEVHNA	276	

Db	227	--PAPELLGSPVFLFPKPKDITLMISITPREVTCVVDVSHEDDEVFNMYVGVGHNA	284
Qy	277	KTKPREQENSPFRVSVYLVTVHQQMLNGKGYKCVSNKGLPASIIEKTI SKTKQPREPQ	336
Db	285	KTKPREQNSTYRVRVSVYLVTVHQQMLNGKGYKCVSNKGLPASIIEKTI SKTKQPREPQ	344
Qy	337	VYVLPSPSRBEMTKNOVSLTCLVKGYPSPDI VEVESNQPPENNYKTPPMLDSDGSFFLY	366
Db	345	VYVLPSPSRBELTKNOVSLTCLVKGYPSPDI VEVESNQPPENNYKTPPVLSDGSFFLY	404
Qy	397	SKLTVDKSRMOQGNVPSGVVHEALAHNYTKSLISLSPGK	436
Db	405	SKLTVDKSRMOQGNVPSGVVHEALAHNYTKSLISLSPGK	444

```

1      RESULT 3
2      US-11-025-712--12
3      / Sequence 12, Application US/11025712
4      / Publication No. US20050255108A1
5      / GENERAL INFORMATION:
6      /   APPLICANT: Bednar, Martin M.
7      /   Thomas, G. Roger
8      /   Gross, Cordell E.
9      /   TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
10     /   NUMBER OF SEQUENCES: 15
11     /   CORRESPONDENCE ADDRESS:
12     /   ADDRESSEE: Genentech, Inc.
13     /   STREET: 1 DNA Way
14     /   CITY: South San Francisco
15     /   STATE: California
16     /   COUNTRY: USA
17     /   ZIP: 94080
18     /   COMPUTER READABLE FORM:
19     /   MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
20     /   COMPUTER: IBM PC compatible
21     /   OPERATING SYSTEM: PC-DOS/MS-DOS
22     /   SOFTWARE: Winpatin (Genentech)
23     /   CURRENT APPLICATION DATA:
24     /   APPLICATION NUMBER: US/11/025,712
25     /   FILING DATE: 28-Dec-2004
26     /   CLASSIFICATION: <Unknown>
27     /   PRIOR APPLICATION DATA:
28     /   APPLICATION NUMBER: US/10/404,286
29     /   FILING DATE: 31-Mar-2003
30     /   APPLICATION NUMBER: 09/811384
31     /   FILING DATE: 20-DEC-2000
32     /   APPLICATION NUMBER: 09/251552
33     /   FILING DATE: 17-FEB-2000
34     /   APPLICATION NUMBER: 08/788800
35     /   FILING DATE: 22-JAN-1997
36     /   APPLICATION NUMBER: 60/093038
37     /   FILING DATE: 23-JAN-1996
38     /   ATTORNEY/AGENT INFORMATION:
39     /   NAME: Evans, David W.
40     /   REGISTRATION NUMBER: NONE
41     /   REFERENCE/DOCKET NUMBER: P1729C2
42     /   TELECOMMUNICATION INFORMATION:
43     /   TELEPHONE: 650/225-1739
44     /   TELEFAX: 650/952-9861
45     /   INFORMATION FOR SEQ ID NO: 12:
46     /   SEQUENCE CHARACTERISTICS:
47     /   LENGTH: 450 amino acids
48     /   TYPE: Amino Acid
49     /   TOPOLOGY: Linear
50     /   SEQUENCE DESCRIPTION: SEQ ID NO: 12:
51     /   US-11-025-712-12

```

	Query Match	53.3%;	Score 1239;	DB 7;	Length 450;
	Best Local Similarity	61.0%;	Pred. No. 3.38-90;		
	Matches 261; Conservative	35;	CasHcids 68;	Indels 64;	Gaps 14;
OY	35 DSRVLEKYLEAKAEINITTCSCAHCSLINENITVPDRKVNYA-WKGMEVG--QQAWEVV 91	:	: :: :	: :	:

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollateral Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:17 ; Search time 117.268 Seconds
(without alignments)
1637.343 Million cell updates/sec

Title: US-10-761-593A-20

Perfect score: 2321

Sequence: 1 MGWHECPAMWMLLSLSLP.....MHEALHMYTKSLSLGK 437

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2321	100.0	437	7	ADM33855 Human HUE
2	2321	100.0	437	8	ADR48986 Human L-V
3	2321	100.0	437	8	ADM47518 Human EPO
4	2321	100.0	437	7	AEAL8935 Human ery
5	2321	100.0	437	7	AEAL8935 Human ery
6	2220	95.6	435	7	ADM33857 Human HUE
7	2220	95.6	435	8	ADR48988 Human L-V
8	2220	95.6	435	8	ADM47520 Human EPO
9	2220	95.6	435	9	AEAL8937 Human ery
10	2220	95.6	435	9	AEAL8937 Human ery
11	2212.5	95.3	436	7	ADM33853 Human HUE
12	2212.5	95.3	436	8	ADR48984 Human ery
13	2212.5	95.3	436	8	ADM47516 Human EPO
14	2212.5	95.3	436	9	AEAL8933 Human ery
15	2212.5	95.3	436	9	AEAL8933 Human ery
16	2160	93.1	441	9	AEAL8933 Human ery
17	2110.5	90.9	428	7	AEAL8933 Human ery
18	2110.5	90.9	428	8	ADM47520 Human EPO
19	2110.5	90.9	428	9	AEAL8933 Human ery
20	2058.5	88.7	420	5	AAE15348 Human ery
21	1961	84.5	425	7	ABU64199 Plasmaid P
22	1961	84.5	425	8	ADO10511 Kd signal
23	1932.5	83.3	444	9	ADV97042 Human EPO
24	1346.5	58.0	449	7	ADM33378 Human GCS

25	1346.5	58.0	449	9	ADV91793
26	1346.5	58.0	449	9	ADV9714 hg-CSF-L-
27	1345	57.9	433	8	ADM50825 Human int
28	1322	57.0	433	2	AAW18579 Interfero
29	1301	56.1	432	2	AAW17903 Human IFN
30	1293.5	55.7	284	6	AAE30927 Gly8-Glu2
31	1256.5	54.1	266	8	AAW52121 Human che
32	1255.5	54.1	326	2	AAW76221 Human che
33	1255.5	54.1	328	2	AAW76220 Human che
34	1251.5	53.9	331	2	AAW76222 Human che
35	1250	53.9	331	2	AAW76223 Human che
36	1245.5	53.7	447	7	ADM33380 Human GCS
37	1245.5	53.7	447	9	ADV91795 Human GCS
38	1245.5	53.7	447	9	ADV9716 hg-CSF-L-
39	1244	53.6	431	8	ADM50827 Human int
40	1243.5	53.6	751	3	AAW11692 Human sec
41	1243.5	53.6	784	3	AAW11694 Human sec
42	1241.5	53.4	403	7	ADD32018 Heterolog
43	1239	53.4	396	2	AAW10535 Leptin 1-
44	1238	53.3	382	2	AAW90922 IL4-Y124D
45	1238	53.3	448	7	ADM33376 Human GCS

ALIGNMENTS

RESULT 1	ADM33855	ADM33855 standard; protein; 437 AA.
XX	ADM33855;	
XX	AC	
XX	DT	03-JUN-2004 (first entry)
XX	DE	Human HUEPO-L-VFcgamma4 fusion protein.
XX	KW	Erythropoietin; EPO; immunoglobulin; IgG;
KW	fragment crystallisation region; Fc; chronic anaemia; renal disease;	
KW	cancer chemotherapy; rheumatoid arthritis; AIDS;	
KW	myelodysplastic syndrome; (HUEPO)-L-VFcgamma4; human.	
XX	OS	Homo sapiens.
OS	OS	Synthetic.
XX	Key	Location/Qualifiers
FT	Peptide	1..27
FT	Protein	28..192
FT	Protein	/note= "EPO"
FT	Peptide	193..208
FT	Protein	/note= "linker"
FT	Protein	209..437
FT	Protein	/note= "IgG4 Fc"
FT	Misc-difference	219
FT	Misc-difference	/note= "Wild-type Ser substituted by Pro"
FT	Misc-difference	226
FT	Misc-difference	/note= "Wild-type Leu substituted by Ala"
XX	US2003082749-A1.	
XX	01-MAY-2003.	
XX	17-AUG-2001; 2001US-00932812.	
XX	17-AUG-2001; 2001US-00932812.	
XX	(SUNL/) SUN L K.	
XX	(SUNB/) SUN B N C.	
XX	(SUNC/) SUN C R Y.	
XX	Sun LK, Sun BNC, Sun CRY;	
XX	WPI; 2003-616080/58.	

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:21 / Search time 21.3823 Seconds

(without alignments)
1966.430 Million cell updates/sec

Title: US-10-761-593a-20

Perfect score: 2321

Sequence: 1 MGVHECPAMWLLSLSLSP.....MEHALNHYTQKSLSLCK 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80:*
2: PIR:*
3: PIR:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1226	52.8	327	1	G4HU	Ig gamma-4 chain C
2	1144	49.3	327	2	S69339	Ig heavy chain V r
3	1138	49.0	255	4	S31866	Ig gamma-1 chain C
4	1138	49.0	330	1	GHHU	Ig gamma-1 chain C
5	1125	48.5	326	1	G2HU	Ig gamma-2 chain C
6	1123	48.4	377	2	A60764	Ig gamma-3 chain C
7	1113	48.0	377	2	A23511	Ig gamma-3 chain C
8	1101	47.4	234	2	PT0207	Ig gamma-1 chain C
9	1095	47.2	289	1	G3HWTI	Ig gamma-3 heavy C
10	994	42.8	193	1	ZUHU	erythropoietin pre
11	916.5	39.5	328	2	I47160	Ig gamma 2b chain
12	916.5	39.5	328	2	I47159	Ig gamma 2a chain
13	908.5	39.1	277	2	I47162	Ig gamma 4 chain C
14	902.5	38.9	192	1	JQ0173	erythropoietin pre
15	897.5	38.7	192	1	I84613	Ig gamma 3 chain C
16	893.5	38.5	328	2	I47161	Ig gamma 3 chain C
17	882	38.0	323	1	GHRB	Ig gamma chain C r
18	878.5	37.9	328	2	I47158	Ig gamma 1 chain C
19	871.5	37.5	470	2	S22080	Ig heavy chain pre
20	851	36.7	329	1	G2GP	Ig gamma-2 chain C
21	850	36.6	472	2	S31459	Ig gamma-1 chain -
22	848	36.5	308	2	C30554	Ig heavy chain C r
23	819.5	35.3	333	2	PS0018	Ig gamma-2b chain
24	815	35.1	329	1	G3MSC	Ig gamma-3 chain C
25	813.5	35.0	444	2	PC4456	monoclonal antibod
26	810.5	34.9	326	2	PS0017	Ig gamma-1 chain C
27	808	34.8	469	2	S37483	Ig gamma-2a chain
28	807	34.8	398	1	G3MSM	Ig gamma-3 chain C
29	803.5	34.6	324	1	G1MS	Ig gamma-1 chain C

30	802	34.6	329	2	S00847	Ig gamma-2c chain
31	798.5	34.4	330	1	G2MSA	Ig gamma-2a chain
32	798.5	34.4	333	1	G1MSM	Ig gamma-1 chain C
33	798	34.4	335	1	G2MSAB	Ig gamma-2a chain
34	797.5	34.4	188	1	I46083	erythropoietin pre
35	793.5	34.2	399	1	G2MSAM	Ig gamma-2a chain
36	783.5	33.8	446	2	S40295	Ig gamma-2a chain
37	773.5	33.3	474	1	G2MS11	Ig gamma-2b chain
38	771.5	33.2	192	1	S28148	erythropoietin pre
39	767.5	33.1	327	2	S06611	Ig gamma-2 chain C
40	765.5	33.0	194	1	I46401	erythropoietin pre
41	765.5	33.0	405	1	G2MSBM	Ig gamma-2b chain
42	764	32.9	322	2	PS0019	Ig gamma-2a chain
43	761.5	32.8	190	2	I46578	erythropoietin pre
44	751.5	32.4	192	1	A24902	erythropoietin pre
45	743.5	32.0	475	2	S01321	Ig gamma-2b chain

ALIGNMENTS

RESULT 1

G4HU
Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence.revision 02-Apr-1982 #ext_change 09-Jul-2004

C/Accession: A90933; A90249; A02150

R/Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Accession: A90933; M01D:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 <ELL>

A/Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A/Note: The sequence was determined from the germline gene

R/Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A/Reference number: A90249; M01D:70207560; PMID:4192699

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-301-326 <PIN>

A/Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796

C/Genetics:

A/Gene: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Intons: 99/1; 111/1; 221/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.

C/Superfamily: Immunoglobulin C region; Immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology <IM1>

F/99-110/Region: hinge

F/134-203/Domain: immunoglobulin homology <IM2>

F/240-307/Domain: immunoglobulin homology <IM3>

F/14/Disulfide bonds: interchain (to light chain) #status experimental

F/27-83,141-201,247-305/Disulfide bonds: #status predicted

F/106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F/177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.8%; Score 1226; DB 1; Length 327;
Best Local Similarity 99.1%; Pred. No. 3.4e-74;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	209	ESKKGPPCPCPAPAFAGGVSFLFPKPKDITMISRTSEVTCVVVDVSGEDPEVQFNWY	268
DB	99	ESKKGPPCPCPAPAFAGGVSFLFPKPKDITMISRTSEVTCVVVDVSGEDPEVQFNWY	158
QY	269	VDGVEVHNATKPREQFNSTYRVSVLVTVLHODMNGKRYCKVSNKGLPSIETIKS	328
DB	159	VDGVEVHNATKPREQFNSTYRVSVLVTVLHODMNGKRYCKVSNKGLPSIETIKS	218

QY 329 AKGQPREPOVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPTPVLT
|||||
Db 219 AKGQPREPOVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPTPVLT 278

QY 389 DSGSFFLYSRLTVDKSRMOEGNVFSCSVNHEALHNHYTQKSLSLSPGK 437
Db 279 DSGSFFLYSRLTVDKSRMOEGNVFSCSVNHEALHNHYTQKSLSLSPGK 327

RESULT 2
Ig heavy chain V region precursor - human
C/Species: Homo sapiens (man)
C/Date: 18-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C/Accession: S69339; S72664
R/Kamlich, A.A.; Accouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229: 34-60, 1995
A/Title: Structure of abdominal heavy chains in human heavy-chain-deposition disease.
A/Reference number: S69339; MUID:95262687; PMID:7744049
A/Accession: S69339
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-374 <KHA>
A/Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R/Kamlich, A.A.
Submitted to the EMBL Data Library, September 1994
A/Reference number: S72664
A/Accession: S72664
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-140, 'C', 142-374 <KH2>
A/Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C/Superfamily: Immunoglobulin C region; Immunoglobulin homology

Query Match 49.3%; Score 1144; DB 2; Length 374;
Best Local Similarity 94.6%; Pred. No. 1.1e-68;
Matches 210; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 216 CPPCPAPBPAAGPSVFLFPKPKDITLMSRTPEVTCVVVDVSOEDPEVFNMYVDGVEVH 275
|||||
Db 153 CPPCPAPBPAAGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 212

QY 276 NAKTKREBOFNSTYRVSVLTVTLHODWLNKGEYKCKVSNKGPPSIIEKTIISKAKQPRE 335
|||||
Db 213 NAKTKREBOFNSTYRVSVLTVTLHODWLNKGEYKCKVSNKGPPSIIEKTIISKAKQPRE 272

QY 336 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPTPVLTDSGSPF 395
Db 273 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPTPVLTDSGSPF 332

QY 396 LYSRLTVDKSRMOEGNVFSCSVNHEALHNHYTQKSLSLSPGK 437
Db 333 LYSRLTVDKSRMOEGNVFSCSVNHEALHNHYTQKSLSLSPGK 374

RESULT 3
Ig gamma-1 chain C region - synthetic
C/Species: synthetic
A/Note: Homo sapiens (man) gene engineered and expressed in *Escherichia coli*.
C/Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C/Accession: S31866
R/Filipula, D.
Submitted to the EMBL Data Library, February 1993
A/Description: Screening method for protein-protein interactions of cloned gene products.
A/Reference number: S31866
A/Accession: S31866
A/Molecule type: mRNA
A/Residues: 1-253 <FIL>
A/Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA9866.1; PID
C/Keywords: Immunoglobulin F/1-22/Region; *Escherichia coli* outer membrane protein A precursor

F/23-255/Region: human Ig gamma-1 chain C region

Query Match 49.0%; Score 1138; DB 4; Length 255;
Best Local Similarity 93.7%; Pred. No. 1.8e-68;
Matches 208; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 216 CPPCPAPBPAAGPSVFLFPKPKDITLMSRTPEVTCVVVDVSOEDPEVFNMYVDGVEVH 275
Db 34 CPPCPAPBPAAGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 93

QY 276 NAKTKREBOFNSTYRVSVLTVTLHODWLNKGEYKCKVSNKGPPSIIEKTIISKAKQPRE 335
Db 94 NAKTKREBOFNSTYRVSVLTVTLHODWLNKGEYKCKVSNKGPPSIIEKTIISKAKQPRE 153

QY 336 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPTPVLTDSGSPF 395
Db 154 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPTPVLTDSGSPF 213

QY 396 LYSRLTVDKSRMOEGNVFSCSVNHEALHNHYTQKSLSLSPGK 437
Db 214 LYSRLTVDKSRMOEGNVFSCSVNHEALHNHYTQKSLSLSPGK 255

RESULT 4
IGHD
Ig gamma-1 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C/Accession: A93433; S36861; S33887; B90563; A90564; B91666; A91723; A02146
R/Elleston, U.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10: 4071-4079, 1982
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A/Reference number: A93433; MUID:82274238; PMID:6287432
A/Accession: A93433
A/Molecule type: DNA
A/Residues: 1-330 <EL>
A/Cross-references: UNIPROT:P01857; UNIPARC:UPI000034COB; EMBL:Z17370
A/Note: this sequence has the Gln(17) alloypic marker, 97-Lys, and the Gln(1) markers,
R/Harris, L.J.
Submitted to the EMBL Data Library, October 1992
A/Reference number: S33904
A/Accession: S36861
A/Molecule type: DNA
A/Residues: 2-330 <HAR>
A/Cross-references: UNIPARC:UPI000013G6FE; EMBL:Z17370
R/Takahashi, N.; Ueda, S.; Obara, M.; Nakado, T.; Nakai, S.; Honjo, T.
Cell 29: 671-679, 1982
A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A/Reference number: S33887; MUID:83001943; PMID:6811139
A/Accession: S33887
A/Molecule type: DNA
A/Residues: 88-113; 235-330 <TXK>
A/Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9: 3161-3170, 1970
A/Title: The covalent structure of a human gammag2-immunoglobulin. VII. Amino acid sequ
A/Reference number: A90563; MUID:71064024; PMID:5489771
A/Accession: B90563
A/Contents: myeloma protein Rn
A/Molecule type: protein
A/Residues: 1-96, 'R', 98-135 <CUN>
A/Cross-references: UNIPARC:UPI000017378D
R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9: 3171-3181, 1970
A/Title: The covalent structure of a human gammag2-immunoglobulin. VIII. Amino acid sequ
A/Reference number: A90564; MUID:71064025; PMID:5530842
A/Accession: B90564
A/Molecule type: protein
A/Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240
A/Cross-references: UNIPARC:UPI000017378E

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 17, 2006, 08:33:16 ; Search time 195.113 Seconds

(without alignments)
1580.190 Million cell updates/sec

Title: US-10-761-593a-20

Perfect score: 2321

Sequence: 1 MGVHBCPALWLLSLSLSLP.....MHKALHNYTKSLSLSLGK 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226	52.8	37	1	IGHG4_HUMAN
2	1226	52.8	473	1	P01861 homo sapien
3	1220	52.6	476	2	O8T6C3 homo sapien
4	1152	49.6	487	2	O6MXZ7_HUMAN
5	1144	49.3	348	2	O65ZL2_MOUSE
6	1144	49.3	473	2	O6PYX1_HUMAN
7	1144	49.3	478	2	O6MZV7_HUMAN
8	1144	49.3	480	2	O6P181_HUMAN
9	1138	49.0	330	1	O6R1P1_HUMAN
10	1138	49.0	465	1	IGHG1_HUMAN
11	1138	49.0	466	2	O6GMX6_HUMAN
12	1138	49.0	469	2	O6IN78_HUMAN
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15	1138	49.0	470	2	O7Z5W1_HUMAN
16	1138	49.0	472	2	O6PUJ4_HUMAN
17	1138	49.0	475	2	O6N089_HUMAN
18	1138	49.0	475	2	O5EFES_HUMAN
19	1138	49.0	475	2	O6GMW7_HUMAN
20	1138	49.0	679	2	O6GMX1_HUMAN
21	1134	48.9	473	2	O96P08_HUMAN
22	1134	48.9	475	2	O6P055_HUMAN
23	1134	48.9	480	2	O6MZ06_HUMAN
24	1134	48.9	481	2	O6N094_HUMAN
25	1134	48.9	482	2	O6N097_HUMAN
26	1131	48.7	466	2	O7Z3S1_HUMAN
27	1130	48.7	544	2	O6N096_HUMAN
28	1127	48.6	475	2	O6P3J5_HUMAN
29	1125.5	48.5	326	2	O6N095_HUMAN
30	1125.5	48.5	417	2	IGHG2_HUMAN
31	1122.5	48.4	464	2	O6N093_HUMAN
					O6MZU6_HUMAN

32	1121	48.3	475	2	O5RE17_PONPY
33	1120.5	48.3	465	2	O6P6C4_HUMAN
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37	1113	48.0	519	2	O5EBM2_HUMAN
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41	994	42.8	193	2	O545U2_HUMAN
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ALIGNMENTS

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AC      P01861;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Ig gamma-4 chain C region.
GN      Name=IGHG4;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=83157104; PubMed=6299662;
RA      Ellison J.W., Buxbaum J.N., Hood L.E.;
RT      "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL      DNA 1:11-18(1981).
RN      [2]
RP      PROTEIN SEQUENCE OF 1-30 AND 81-326.
RX      MEDLINE=70207560; PubMed=4192699;
RA      Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT      "Human immunoglobulin subclasses. Partial amino acid sequence of the
      constant region of a gamma 4 chain.";
RL      Biochem. J. 117:33-47(1970).
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; K01316; AAB59394.1; ALT_INIT; Genomic_DNA.
DR      PIR; A90933; GAHU.
DR      PDB; 1ADQ; X-ray; A=118-323.
DR      SRR; P01861; 1-327.
DR      HGNC; HGNC:5528; IGHG4.
DR      MIM; 147130; -.
DR      GO; GO:0005624; C:membrane fraction; NAS.
DR      GO; GO:0003823; F:antigen binding; TAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; Pf07654; C1-set; 3.
DR      SMART; SM00407; IgC1; 2.
DR      PROSITE; PSS00835; IG_LIKE; 3.
DR      PROSITE; PSS00290; IG_MHC; 2.
KW      3D-structure; Direct protein sequencing; Immunoglobulin C region;
KW      Immunoglobulin domain.
FT      REGION      1      98      CH1.
FT      REGION      99      110      Hinge.

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FT REGION 111 220 CH2.
 FT REGION 221 327 CH3.
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 FT DISULFID 27 83 Interchain (with a heavy chain).
 FT DISULFID 106 106 Interchain (with a heavy chain).
 FT DISULFID 109 109 Interchain (with a heavy chain).
 FT DISULFID 141 201
 FT DISULFID 247 305
 FT NON_TER 1
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Query Match 52.8%; Score 1226; DB 1; Length 327;
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 QY 269 VDGVEVHNAKTKRREQFSTYRVSVLTFLHODMNLGKREYKCKVSNKGLPSSIEKTIK 328
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 DB 219 AKGQPREPVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVL 278
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 DB 279 DSDGSFELYSLTVDKSRWQGNVFSQVMHEALHNHYTQKSLSLSTGK 327

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 ID Q8T633_HUMAN PRELIMINARY; PRT; 473 AA.

AC Q8T633; Feingold E.A., Grouse L.H., Derge J.G.,
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHG4 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,
 RA Datchenko L., Marusik K., Farmer A.T., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Richards S., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Whiting M., Maden A., Young A.C., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Schnerbach A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "generation and initial analysis of more than 15,000 full-length human
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Strauberg R.,

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025985; AAH25985.1; -, mRNA.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR007110; IG_1-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 52.8%; Score 1226; DB 2; Length 473;
 Best Local Similarity 99.1%; Pred. No. 7.4e-82;
 Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 209 ESKYGPCCPCPAPAEFAGPSVFLFPPKPKDTLMTISRTPEVTCVVVDVSOEDPEVQFNMY 268
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 QY 269 VDGVEVHNAKTKRREQFSTYRVSVLTFLHODMNLGKREYKCKVSNKGLPSSIEKTIK 328
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RESULT 3

Q6MZK7 HUMAN
 ID Q6MZK7_HUMAN PRELIMINARY; PRT; 476 AA.

AC Q6MZK7; Feingold E.A., Grouse L.H., Derge J.G.,
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686M24218;
 GN Name=DKFZp686M24218;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human rectum tumor;
 RA The German Human cDNA Consortium;
 RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobio G., Har M., Wiemann S.,
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640824; CAB45900.1; -, mRNA.
 DR HSSP; P01861; IADQ.
 DR SWR; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 3.
 DR SMART; SM00409; IGV; 2.
 DR SMART; SM00407; IG_C1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:24 ; Search time 56.7966 Seconds
(without alignments)
636.116 Million cell updates/sec

Title: US-10-761-593A-20
Perfect score: 2321
Sequence: 1 MGVHECPAMLMILLSTLSPMEBALHHYTKSLSTSLGK 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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6: /csm2_6/prodata1/1aa/backfill1.rep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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2	2320	99.6	435	2	US-09-932-812A-22	Sequence 22, Appl1
3	2212.5	99.3	436	2	US-09-932-812A-18	Sequence 18, Appl1
4	1346.5	95.0	449	2	US-09-966-362A-20	Sequence 20, Appl1
5	1255.5	54.1	326	2	US-08-808-720-3	Sequence 3, Appl1
6	1255.5	54.1	326	2	US-09-467-638-3	Sequence 3, Appl1
7	1255.5	54.1	326	2	US-08-808-720-1	Sequence 1, Appl1
8	1255.5	54.1	328	2	US-09-467-638-1	Sequence 1, Appl1
9	1251.5	53.9	331	2	US-08-808-720-5	Sequence 5, Appl1
10	1251.5	53.9	331	2	US-09-467-638-5	Sequence 5, Appl1
11	1250	53.9	331	2	US-08-808-720-7	Sequence 7, Appl1
12	1250	53.9	331	2	US-09-467-638-7	Sequence 7, Appl1
13	1245.5	53.7	447	2	US-09-966-362A-22	Sequence 22, Appl1
14	1238	53.3	382	1	US-08-470-299-10	Sequence 10, Appl1
15	1238	53.3	448	2	US-09-966-362A-18	Sequence 18, Appl1
16	1237.5	53.3	917	2	US-10-282-162-56	Sequence 56, Appl1
17	1234	53.2	460	2	US-10-630-406-5	Sequence 5, Appl1
18	1234	53.2	467	2	US-08-523-894-12	Sequence 12, Appl1
19	1234	53.2	902	2	US-10-282-162-38	Sequence 38, Appl1
20	1234	53.2	902	2	US-10-282-162-44	Sequence 44, Appl1
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22	1230	53.0	382	1	US-08-470-299-7	Sequence 7, Appl1
23	1229.5	53.0	917	2	US-10-282-162-54	Sequence 54, Appl1
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25	1226	52.8	229	2	US-08-761-277A-47	Sequence 47, Appl1
26	1226	52.8	329	2	US-09-313-942-12	Sequence 12, Appl1
27	1226	52.8	329	2	US-09-313-942-12	Sequence 12, Appl1

ALIGNMENTS

28	1226	52.8	329	2	US-10-289-182-12	Sequence 12, Appl
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31	1226	52.8	467	2	US-08-523-894-8	Sequence 8, Appl
32	1226	52.8	467	2	US-08-523-894-10	Sequence 10, Appl
33	1226	52.8	502	2	US-10-288-162-36	Sequence 36, Appl
34	1226	52.8	502	2	US-10-288-162-42	Sequence 42, Appl
35	1226	52.8	502	2	US-10-288-162-48	Sequence 48, Appl
36	1226	52.8	917	2	US-07-91-098A-45	Sequence 45, Appl
37	1209.5	52.1	967	1	US-09-227-595-28	Sequence 28, Appl
38	1205.5	51.9	374	2	US-09-227-595-86	Sequence 26, Appl
39	1205.5	51.9	374	2	US-08-595-5908-26	Sequence 26, Appl
40	1205.5	51.9	374	2	US-08-595-5908-28	Sequence 28, Appl
41	1180.5	50.9	269	2	US-09-428-0828-10	Sequence 10, Appl
42	1180.5	50.9	277	2	US-09-428-0828-20	Sequence 20, Appl
43	1180.5	50.8	1558	2	US-09-313-942-26	Sequence 26, Appl
44	1178.5	50.8	1158	2	US-10-288-162-36	Sequence 26, Appl
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RESULT 1
US-09-932-812A-20
/ Sequence 20, Application US/09932812A
/ Patent No. 6900292
/ GENERAL INFORMATION:
/ APPLICANT: Sun, Lee-Hwei K
/ APPLICANT: Sun, Bill N
/ APPLICANT: Sun, Cecily R
/ TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
/ TITLE OF INVENTION: increased biological
/ FILE REFERENCE: 02SDN2001
/ CURRENT APPLICATION NUMBER: US/09/932,812A
/ CURRENT FILING DATE: 2001-08-17
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 20
/ LENGTH: 437
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide
/ OTHER INFORMATION: (Figure 2B
/ OTHER INFORMATION: )
US-09-932-812A-20

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Query Match	100.0%;	Score 2321;	DB 2;	Length 437;
Best Local Similarity	100.0%;	Pred. No. 3.4e-197;		
Matches 437; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

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Db	61	SLNENITVPDPTKVNFYAMKRMVEVGOAOAVEWOGALLSEAVLRGQALLVNSSPWEPLQ	120
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QY	181	KLYTGACRTGGSGGGSGGGSGGGSGGSESKTGPCPCPAPAFAGPSVFLPPPKKDT	240
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DB 301 QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPOVYTLPPSQEEMTKNQVSLTCLVK 360
QY 361 GFFPSDIAVWESNNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQGAGVFNFSQMYH 420
DB 361 GFFPSDIAVWESNNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQGAGVFNFSQMYH 420
QY 421 ALHNHYTQKSLSLSPGK 437
DB 421 ALHNHYTQKSLSLSPGK 437

RESULT 2
US-09-932-812A-22
; Sequence 22, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HWP0-L-vFc gamma1 with a 27-amino acid leader peptide
; OTHER INFORMATION: (Figure 2C
; OTHER INFORMATION:)
US-09-932-812A-22

Query Match 95.6%; Score 2220; DB 2; Length 435;
Best Local Similarity 95.7%; Pred. No. 3e-188; 7; Indels 2; Gaps 1;
Matches 418; Conservative 10; Mismatches
QY 1 MGVECPAMLMILLISLPLGLPVGAAPRLICDSRVLEERYLLLEAKEAENITTCGAHRC 60
DB 1 MGVECPAMLMILLISLPLGLPVGAAPRLICDSRVLEERYLLLEAKEAENITTCGAHRC 60
QY 61 SINENITVPDPTKYNFYAMKMEVGOQAVEMOGIALLSAVLRGQALLVNSQPMPELQL 120
DB 61 SINENITVPDPTKYNFYAMKMEVGOQAVEMOGIALLSAVLRGQALLVNSQPMPELQL 120
QY 121 HDKAVSGLSLTTLRLALGAQKEAISPPDAASAAPRTITADTFPKLFRVYSNFIKGL 180
DB 121 HDKAVSGLSLTTLRLALGAQKEAISPPDAASAAPRTITADTFPKLFRVYSNFIKGL 180
QY 121 KLTGACRTGDSGGSGGGSGGSGGSGSKYGPCCPAPAFAGSPVFLFPPPKDPT 240
DB 121 KLTGACRTGDSGGSGGGSGGSGGSGSKYGPCCPAPAFAGSPVFLFPPPKDPT 240
QY 181 KLTGACRTGDSGGSGGGSGGSGGSGSKYGPCCPAPAFAGSPVFLFPPPKDPT 240
DB 181 KLTGACRTGDSGGSGGGSGGSGGSGSKYGPCCPAPAFAGSPVFLFPPPKDPT 240
QY 241 LMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKTRPREEQFNSTYRVVSVLTVLA 300
DB 241 LMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKTRPREEQFNSTYRVVSVLTVLA 300
QY 301 QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPOVYTLPPSQEEMTKNQVSLTCLVK 360
DB 301 QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPOVYTLPPSQEEMTKNQVSLTCLVK 360
QY 361 GFFPSDIAVWESNNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQGAGVFNFSQMYH 420
DB 361 GFFPSDIAVWESNNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQGAGVFNFSQMYH 420
QY 421 ALHNHYTQKSLSLSPGK 437
DB 421 ALHNHYTQKSLSLSPGK 437

DB 419 ALHNHYTQKSLSLSPGK 435

RESULT 3
US-09-932-812A-18
; Sequence 18, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HWP0-L-vFc gamma2 with a 27-amino acid leader peptide
; OTHER INFORMATION: (Figure 2
; OTHER INFORMATION: A)
US-09-932-812A-18

Query Match 95.3%; Score 2212.5; DB 2; Length 436;
Best Local Similarity 95.9%; Pred. No. 1.4e-187;
Matches 419; Conservative 10; Mismatches 10; Indels 1; Gaps 1;
QY 1 MGVECPAMLMILLISLPLGLPVGAAPRLICDSRVLEERYLLLEAKEAENITTCGAHRC 60
DB 1 MGVECPAMLMILLISLPLGLPVGAAPRLICDSRVLEERYLLLEAKEAENITTCGAHRC 60
QY 61 SINENITVPDPTKYNFYAMKMEVGOQAVEMOGIALLSAVLRGQALLVNSQPMPELQL 120
DB 61 SINENITVPDPTKYNFYAMKMEVGOQAVEMOGIALLSAVLRGQALLVNSQPMPELQL 120
QY 121 HDKAVSGLSLTTLRLALGAQKEAISPPDAASAAPRTITADTFPKLFRVYSNFIKGL 180
DB 121 HDKAVSGLSLTTLRLALGAQKEAISPPDAASAAPRTITADTFPKLFRVYSNFIKGL 180
QY 181 KLTGACRTGDSGGSGGGSGGSGGSGSKYGPCCPAPAFAGSPVFLFPPPKDPT 240
DB 181 KLTGACRTGDSGGSGGGSGGSGGSGSKYGPCCPAPAFAGSPVFLFPPPKDPT 240
QY 241 LMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKTRPREEQFNSTYRVVSVLTVLA 300
DB 241 LMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKTRPREEQFNSTYRVVSVLTVLA 300
QY 301 QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPOVYTLPPSQEEMTKNQVSLTCLVK 360
DB 301 QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPOVYTLPPSQEEMTKNQVSLTCLVK 360
QY 361 GFFPSDIAVWESNNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQGAGVFNFSQMYH 420
DB 361 GFFPSDIAVWESNNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQGAGVFNFSQMYH 420
QY 421 ALHNHYTQKSLSLSPGK 437
DB 421 ALHNHYTQKSLSLSPGK 436

RESULT 4
US-09-968-362A-20
; Sequence 20, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2006, 08:42:04 ; Search time 42.0963 Seconds
(without alignments)
441.079 Million cell updates/sec

Title: US-10-761-593A-20

Perfect score: 2321
Sequence: 1 MGWHECPAWMLLSTLSLP.....MHEALNHVTKSLSLGK 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
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2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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4: /SIDS5/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2110.5	90.9	428	US-11-029-003-24	Sequence 24, Appl
2	1932.5	83.3	444	US-11-029-003-16	Sequence 16, Appl
3	1240	53.4	497	US-11-274-344-17	Sequence 17, Appl
4	1237.5	53.3	917	US-11-144-987-26	Sequence 26, Appl
5	1237.5	53.3	917	US-11-205-935-26	Sequence 26, Appl
6	1234	53.2	434	US-11-204-709-24	Sequence 24, Appl
7	1234	53.2	902	US-11-144-987-8	Sequence 8, Appl
8	1234	53.2	902	US-11-144-987-14	Sequence 14, Appl
9	1234	53.2	902	US-11-205-935-8	Sequence 8, Appl
10	1234	53.2	902	US-11-205-935-14	Sequence 14, Appl
11	1234	53.2	917	US-11-144-987-20	Sequence 20, Appl
12	1234	53.2	917	US-11-205-935-20	Sequence 20, Appl
13	1229.5	53.0	917	US-11-205-935-24	Sequence 24, Appl
14	1229.5	53.0	917	US-11-205-935-24	Sequence 24, Appl
15	1226	52.8	327	US-10-999-866-38	Sequence 38, Appl
16	1226	52.8	327	US-10-988-207-22	Sequence 22, Appl
17	1226	52.8	327	US-10-493-909-26	Sequence 26, Appl
18	1226	52.8	327	US-10-935-005B-69	Sequence 69, Appl
19	1226	52.8	327	US-11-061-821-38	Sequence 38, Appl
20	1226	52.8	327	US-11-102-621-114	Sequence 114, Appl
21	1226	52.8	327	US-11-124-620-4	Sequence 4, Appl
22	1226	52.8	327	US-11-233-683-4	Sequence 4, Appl
23	1226	52.8	328	US-10-988-207-23	Sequence 23, Appl
24	1226	52.8	329	US-11-122-622-100	Sequence 100, Appl
25	1226	52.8	451	US-11-166-906-1	Sequence 1, Appl

26	1226	52.8	626	7	US-11-050-346-19	Sequence 19, Appl
27	1226	52.8	864	7	US-11-050-346-10	Sequence 10, Appl
28	1226	52.8	864	7	US-11-103-077-29	Sequence 29, Appl
29	1226	52.8	902	7	US-11-144-987-6	Sequence 6, Appl
30	1226	52.8	902	7	US-11-144-987-12	Sequence 12, Appl
31	1226	52.8	902	7	US-11-205-935-6	Sequence 6, Appl
32	1226	52.8	902	7	US-11-205-935-12	Sequence 12, Appl
33	1226	52.8	917	7	US-11-144-987-18	Sequence 18, Appl
34	1226	52.8	917	7	US-11-205-935-18	Sequence 18, Appl
35	1223	52.7	337	7	US-11-102-621-116	Sequence 116, Appl
36	1223	52.7	451	7	US-11-102-621-144	Sequence 144, Appl
37	1221	52.6	326	6	US-10-988-207-24	Sequence 24, Appl
38	1220.5	52.6	430	6	US-11-029-003-22	Sequence 22, Appl
39	1220	52.6	451	7	US-11-102-621-142	Sequence 142, Appl
40	1220	52.6	451	7	US-11-102-621-143	Sequence 143, Appl
41	1217	52.4	337	7	US-11-102-621-117	Sequence 117, Appl
42	1217	52.4	451	7	US-11-102-621-145	Sequence 145, Appl
43	1215	52.3	451	7	US-11-102-621-146	Sequence 146, Appl
44	1204.5	51.9	249	6	US-10-935-005B-89	Sequence 89, Appl
45	1201.5	51.8	247	6	US-10-935-005B-87	Sequence 87, Appl

ALIGNMENTS

```
RESULT 1
US-11-029-003-24
; Sequence 24, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTTEL, JAMES
; TITLE OF INVENTION: IMMONOGLLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-029-003-24
Query Match          90.9%;   Score 2110.5;   DB 7;   Length 428;
Best local Similarity 91.8%;   Pred. No. 2.2e-156;
Matches 401;   Conservative 9;   Mismatches 18;   Indels 9;   Gaps 1;
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QY	1	MGWHECPAWMLLSTLSLPGLGVPVLCAPRLICDSVRLRYLLAKEAENITTCAGHC	60
DB	1	MGWHECPAWMLLSTLSLPGLGVPVLCAPRLICDSVRLRYLLAKEAENITTCAGHC	60
QY	61	SLNENITVPPTKVFYAKKMEVGOQAVEWQGLALSEAVLRQALLVNSSQWPEPLQ	120
DB	61	SLNENITVPPTKVFYAKKMEVGOQAVEWQGLALSEAVLRQALLVNSSQWPEPLQ	120
QY	121	HYDKAVGSLSTLTLLAALAKOKAISPDAASAPRTTADPFRKLFVYSNPLRGKL	180
DB	121	HYDKAVGSLSTLTLLAALAKOKAISPDAASAPRTTADPFRKLFVYSNPLRGKL	180
QY	181	KLYTGEACRTGDSGGSGGGSGGGSGGSESKYGPCCPAEPAGPVSFLFPKPKDT	240

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Db      181 KLTGACRGTGDEPAAAVDK-----THTCPCPAPBELLGSPSFLFPPKPCOT 231
Qy      241 LMTSRPEYTCVVDVSGEDPEVOFMVYVGVHNAKTPREPOFSTYRVSVLTVLH 300
Db      232 LMTSRPEYTCVVDVSHEDPEVAFNMVYDGVHNAKTPREBQINSTRVSVLTVLH 291
Qy      301 QDWLNKEKYCKKSNKLBESSIEKTIISKAGOPREPOVYTLPPSOEEMTKOVSLTCLYK 360
Db      292 QDWLNKEKYCKKSNKLPAPIEKTIISKAGOPREPOVYTLPPSREBLTKOVSLTCLYK 351
Qy      361 GEPYSDIAVWESNGOPENNKTTPPVLDSDGSFFLYSLRTVDSKRWQEGNVSCSVME 420
Db      352 GEPYSDIAVWESNGOPENNKTTPPVLDSDGSFFLYSKLTVDSKRWQEGNVSCSVME 411
Qy      421 ALHNHYTKSLSLSLGK 437
Db      412 ALHNHYTKSLSLSPGK 428
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RESULT 2

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US-11-029-003-16
; Sequence 16, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029, 003
; PRIOR FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539, 207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487, 964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469, 600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-029-003-16
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Query Match 83.3%; Score 1932.5; DB 7; Length 444;

Best Local Similarity 82.4%; Pred. No. 1.5e-142; Indels 47; Gaps 3;

Matches 379; Conservative 10; Mismatches 24;

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Qy      7 PAWLMLLSLSLPLGLPV-LGAPRLICDSRVLYLLEAKENITTCGAHCSINEN 65
Db      3 PCTLLILIAALATQTTRAGSRAPRLICDSRVLYLLEAKENITTCGAHCSINEN 62
Qy      66 ITVPDTKYNFYAMKMEVGOAVVWQGLLSEAVLRGQALLVNSSQWPEPIQLHVDKA 125
Db      63 ITVPDTKYNFYAMKMEVGOAVVWQGLLSEAVLRGQALLVNSSQWPEPIQLHVDKA 122
Qy      126 VSGLRSLTTLRALGAQKEAISPDAASAPLRTITADTFKLPFRVYSNFRGLKLYTG 185
Db      123 VSGLRSLTTLRALGAQKEAISPDAASAPLRTITADTFKLPFRVYSNFRGLKLYTG 182
Qy      186 EACRTGGSGGG-----SGGGSGGGSGSGSKYGPCCP 217
Db      183 EACRTGGSGGG-----SGGGSGGGSGSGSKYGPCCP 216
Qy      218 PCPAPBEAGGGSVFLFPKPKDITMISRTPEVTCVVVDVSOEDPEVOFNNYVDGVEVNA 277
Db      218 PCPAPBEAGGGSVFLFPKPKDITMISRTPEVTCVVVDVSOEDPEVOFNNYVDGVEVNA 277
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Db      227 ---PAPBELLGSPVFLFPPKPCOTLMISRTPEVTCVVVDVSHEDPEVAFNMVYDGVHNA 284
Qy      278 KTKPREOPNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAGCPREPO 337
Db      285 KTKPREOPNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTIISKAGCPREPO 344
Qy      338 VYTLPPSOEEMTKOVSLTCLYKGFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLY 397
Db      345 VYTLPPSREBLTKOVSLTCLYKGFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLY 404
Qy      398 SRLTVDSKRWQEGNVSCSVMEHALHNHYTKSLSLSLGK 437
Db      405 SKLTVDSKRWQEGNVSCSVMEHALHNHYTKSLSLSPGK 444
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RESULT 3

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US-11-274-344-17
; Sequence 17, Application US/11274344
; Publication No. US20060067920A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Michael
; TITLE OF INVENTION: Chimeric Immunoceptor Useful in Treating Human Cancers
; FILE REFERENCE: 1954-472
; CURRENT APPLICATION NUMBER: US/11/274, 344
; PRIOR FILING DATE: 2005-11-16
; PRIOR APPLICATION NUMBER: 60/286, 981
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 10/134, 645
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-274-344-17
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Query Match 53.4%; Score 1240; DB 7; Length 497;

Best Local Similarity 73.4%; Pred. No. 1.1e-88; Indels 25; Gaps 5;

Matches 248; Conservative 15; Mismatches 50;

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Qy      105 QALLVNSSQWPEPIQLHVDKAVSGLRSLTTL-LRALGAQKEAISP-PDAASAPLRTI 160
Db      46 KAPLCNGSMWMS-INLTAGVYCAALBSLINVSCSAIEKTQRMVLSGCPHKVAGGFSSL 104
Qy      161 -TADTFKLPFRVYSNFRGLKLYTGACRTGDSGGSGGGSGGGSGSKYGPCCP 219
Db      105 HVADTKIEVAQFVKDILLHKKLF-----RGRFNSKYGPCPCPC 145
Qy      220 PAFEPAGGSVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVOFNNYVDGVEVNAKT 279
Db      146 PAFEPAGGSVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVOFNNYVDGVEVNAKT 205
Qy      280 KPREBOPNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAGCPREPO 339
Db      206 KPREBOPNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAGCPREPO 265
Qy      340 TLPPSOEEMTKOVSLTCLYKGFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLYSR 399
Db      266 TLPPSOEEMTKOVSLTCLYKGFYPSDIAVWESNGOPENNKTTPPVLDSDGSFFLYSR 325
Qy      400 LTVDSKRWQEGNVSCSVMEHALHNHYTKSLSLSLGK 437
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RESULT 4

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US-11-144-987-26
; Sequence 26, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
; APPLICANT: Mellif, Scott
; APPLICANT: Karow, Margaret
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Page 2

RESULT 2
 US-10-761-593A-20
 ; Sequence 20, Application US/10761593A
 ; Publication No. US20040175824A1
 ; EXAMINATION SECTION: Hwe1 K
 ; APPLICANT: Sun, Cecily R
 ; APPLICANT: Sun, Cecily R
 ; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological

Query Match	100.0%	Score 2321, DB 4,	Length 437;
Best Local Similarity	100.0%	Pred. No. 3.1e-153;	
Matches 437; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

Db 421 ALHNHYTQKSLSLGLK 437

Query Match	100.0%	Score 2321	DB 6	Length 437
Best Similarity	100.0%	Pred. No. 3.1e-153		
Best Local	0	Mismatches 0	Indels 0	Gaps 0
Match 437	0			

RESULT 4
US-11-017-185-20

1 TITLE OF INVENTION: activities

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2006, 08:33:17 ; Search time 116.732 Seconds
(without alignments)
1637.343 Million cell updates/sec

Title: US-10-761-593A-22

Perfect score: 2312

Sequence: 1 MGVECPAMWLILSLSLSP.....WHEALHNYTKSLSPCK 435

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2312	100.0	435	7	ADM33857	Adm33857 Human HUB
2	2312	100.0	435	8	ADR48988	Adr48988 HUBPO-L-V
3	2312	100.0	435	8	ADM47520	Adm47520 Human EPO
4	2312	100.0	435	9	AEA18937	Aea18937 Human ery
5	2312	100.0	435	9	AEA88757	Aea88757 Human ery
6	2236	96.7	441	9	AEF70229	Aef70229 EPO analo
7	2220	96.0	437	7	ADM33855	Adm33855 Human HUB
8	2220	96.0	437	8	ADR48986	Adr48986 HUBPO-L-V
9	2220	96.0	437	8	ADM47518	Adm47518 Human EPO
10	2220	96.0	437	9	AEA18935	Aea18935 Human ery
11	2220	96.0	437	9	AEA88755	Aea88755 Human ery
12	2216.5	95.9	436	7	ADM33853	Adm33853 Human HUB
13	2216.5	95.9	436	8	ADR48984	Adr48984 HUBPO-L-F
14	2216.5	95.9	436	8	ADM47516	Adm47516 Human EPO
15	2216.5	95.9	436	9	AEA18933	Aea18933 Human ery
16	2216.5	95.9	436	9	AEA88753	Aea88753 Human ery
17	2197.5	95.0	428	7	ADU64200	Adu64200 Plasmid P
18	2197.5	95.0	428	9	ADO10513	Ado10513 EPO sigma
19	2197.5	95.0	428	9	ADV97050	Adv97050 Human Ery
20	2144.5	92.8	420	5	AAE15348	Aae15348 Human ery
21	2048	88.6	425	7	ABU64199	Abu64199 Plasmid P
22	1983.5	85.8	445	8	ADO10511	Ado10511 Kb signal
23	1983.5	85.8	444	9	ADV97042	Adv97042 Human EPO
24	1337.5	57.9	447	7	ADM33380	Adm33380 Human GCS

25	1337.5	57.9	447	9	ADV91795	Adv91795 Human GCS
26	1337.5	57.9	447	9	ADV9716	Adv9716 HG-CSF-L
27	1336	57.8	431	8	ADM50827	Adm50827 Human Int
28	1308.5	56.6	430	9	ADV97048	Adv97048 Human IFN
29	1307	56.5	358	9	AEA46697	Aea46697 Human FSH
30	1297.5	56.1	377	9	AEA46699	Aea46699 Human FSH
31	1293	55.9	513	5	ABG73586	Abg73586 Human End
32	1281	55.4	294	6	AAE30929	Aae30929 G1Y8-Glu2
33	1281	55.4	302	6	AAE30928	Aae30928 G1Y8-Glu2
34	1276	55.2	287	6	AAE30934	Aae30934 Exendin-4
35	1276	55.2	287	6	AAE30926	Aae30926 G1Y8-Glu2
36	1276	55.2	287	6	AAE30931	Aae30931 G1Y8-Glu2
37	1268.5	54.9	269	3	ABE16960	Abb16960 TMP-TMP-F
38	1268.5	54.9	269	5	ABE73413	Abb73413 TMP-TMP-F
39	1268.5	54.9	281	9	ABE7537	Abb7537 Amio ac1
40	1265.5	54.7	277	3	ABE16966	Abb16966 EMP-EMP-F
41	1265	54.7	347	8	ADJ96012	Adj96012 Immunoglo
42	1264	54.7	250	3	ABE17958	Abb17958 MMP inh1b
43	1264	54.7	250	5	ABE73426	Abb73426 MMP inh1b
44	1263.5	54.6	484	5	AAU76916	Aau76916 Human zcy
45	1263.5	54.6	484	6	AAE30844	Aae30844 Human Zcy

ALIGNMENTS

RESULT 1	ADM33857	standard, protein, 435 AA.
ID	ADM33857	standard, protein, 435 AA.
AC	ADM33857;	
XX		
DT	03-JUN-2004	(first entry)
XX		
DE	Human HUBPO-L-VFcgamma1 fusion protein.	
XX		
KW	Erythropoietin; EPO; immunoglobulin; IgG;	
KW	fragment crystallisation region; Fc; chronic anaemia; renal disease;	
KW	cancer chemotherapy; rheumatoid arthritis; AIDS;	
KW	myelodysplastic syndrome; (HUBPO)-L-VFcgamma1; human.	
XX		
OS	Homo sapiens.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..27 "Signal peptide"
FT	Protein	28..192
FT		/note="EPO"
FT	Peptide	193..208
FT	Protein	209..435
FT		/note="IgG1 Fc"
FT	Misc-difference	222
FT		/note="Wild-type Leu substituted by Val"
FT	Misc-difference	318
FT		/note="Wild-type Leu substituted by Ala"
PN	US2003082749-A1.	
PD	01-MAY-2003.	
XX		
PF	17-AUG-2001; 2001US-00932812.	
XX		
PR	17-AUG-2001; 2001US-00932812.	
XX		
PA	(SUNL/) SUN L K.	
PA	(SUNB/) SUN B N C.	
PA	(SUNC/) SUN C R Y.	
XX		
PI	Sun LK, Sun BNC, Sun CRY,	
XX		
DR	WPI, 2003-616080/58.	

DR N-PSDB; ADM33856.

XX New recombinant human erythropoietin-L-vFc fusion proteins, useful for
PT treating patients with chronic anemia caused by renal failure, cancer
PT chemotherapy, rheumatoid arthritis, or azathioprine treatment for HIV
PT infection.

XX Claim 5; Fig 2C; 14pp; English.

XX The invention relates to a recombinant human erythropoietin (HuEPO)-L-vFc
XX fusion protein comprising HuEPO, a peptide linker, and a human
XX immunoglobulin G Fc (fragment crystallisation region) variant. Also
XX included is a carbohydrate-derived cell line producing the human
XX erythropoietin-L-vFc fusion protein cited above in its growth medium in
XX excess of 10 microgramme per million cells in a 24-hour period. The HuEPO
XX -L-vFc fusion protein exhibits an enhanced in vitro biological activity
XX of at least 2-fold relative to that of recombinant HuEPO on a molar
XX basis. The flexible peptide linker containing about 20 or fewer amino
XX acids is present between HuEPO and the human IgG Fc variant. The IgG Fc
XX contains amino acid mutations to attenuate effector functions. The human
XX IgG Fc variant comprises a hinge, CH2 and CH3 domains of human IgG2 with
XX Pro31Ser mutation, human IgG4 with Ser228Pro and Leu235Ala mutations, or
XX human IgG1 with Leu234Val, Leu235Ala and Pro31Ser mutations. The
XX recombinant human erythropoietin-L-vFc fusion proteins are useful for
XX treating patients with chronic anaemia caused by renal failure, cancer
XX chemotherapy, rheumatoid arthritis, azathioprine treatment for HIV
XX infection, or myelodysplastic syndrome. The increased activity and
XX prolonged presence of the human erythropoietin-L-vFc fusion protein in
XX the serum as compared to prior art, leads to lower dosages and less
XX frequent injections. Less fluctuations of the drug in serum
XX concentrations means improved safety and tolerability, and less frequent
XX injections result in better patient compliance and quality of life. The
XX present sequence represents the fusion protein HuEPO-L-vFc-gamma1.

XX Sequence 435 AA;

XX Query Match 100.0%; Score 2312; DB 7; Length 435;

XX Best Local Similarity 100.0%; Pred. No. 66-143; Indels 0; Gaps 0;

XX Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVECPAMWMLLLSLSLPLGLPVGAPRLICDSRVLEKYLEAKENITTCQAHC 60
DB 1 MGVECPAMWMLLLSLSLPLGLPVGAPRLICDSRVLEKYLEAKENITTCQAHC 60
QY 61 SLNENITVDPPTKVFYAMKMEVGQAQAVEVQGIALLSEAVLRGQALLVNSQGPWEPLQI 120
DB 61 SLNENITVDPPTKVFYAMKMEVGQAQAVEVQGIALLSEAVLRGQALLVNSQGPWEPLQI 120
QY 121 HDVKAASGLRSLTTLRALGAQKEAISPDPAAAPLRTITADTFKLFVYNSFLRGKI 180
DB 121 HDVKAASGLRSLTTLRALGAQKEAISPDPAAAPLRTITADTFKLFVYNSFLRGKI 180
QY 181 KLTGTGACRTGDSGGSGSGSGSGSDTHTCCPPAPAEVAGSPVLFPPKPDITLM 240
DB 181 KLTGTGACRTGDSGGSGSGSGSGSDTHTCCPPAPAEVAGSPVLFPPKPDITLM 240
QY 241 ISRTPEVTGVVVVSHEDPEVKFNMYVDGVEVNAKTPKEEYNSITRVASVLTVLHOD 300
DB 241 ISRTPEVTGVVVVSHEDPEVKFNMYVDGVEVNAKTPKEEYNSITRVASVLTVLHOD 300
QY 301 WLNKGKCKVSKKALPASIEKITSKAKGQPREPOVYTLTPSSDELTKNQVSLTCLVKGF 360
DB 301 WLNKGKCKVSKKALPASIEKITSKAKGQPREPOVYTLTPSSDELTKNQVSLTCLVKGF 360
QY 361 YPEDIIVEMSNQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRMOQGNVFSQVMEAL 420
DB 361 YPEDIIVEMSNQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRMOQGNVFSQVMEAL 420
QY 421 HHNYTOKSLSTSPCK 435
DB 421 HHNYTOKSLSTSPCK 435

RESULT 2
ADRA8988
ID ADRA8988 standard; protein; 435 AA.

AC ADRA8988;

DT 02-DEC-2004 (first entry)

DE HuEPO-L-vFc fusion protein #2.

KW anti-anaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;
KW anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
KW AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.

XX Homo sapiens.

OS Synthetic.

PN US2004175824-A1.

PD 09-SEP-2004.

PF 21-JAN-2004; 2004US-00761593.

PR 17-AUG-2001; 2001US-00932812.

XX (SUNL/) SUN L K.

PA (SUNB/) SUN B N C.

PA (SUNC/) SUN C R Y.

XX Sun LK, Sun BNC, Sun CRY;

XX WPI; 2004-634651/61.

DR N-PSDB; ADRA8987.

PT New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
PT (HuEPO), a peptide linker, and a human IgG Fc variant, useful for
PT treating chronic anemia due to renal diseases, cancer chemotherapy, or
PT rheumatoid arthritis.

PS Claim 5; SEQ ID NO 22; 31pp; English.

XX A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
XX (HuEPO), a peptide linker, and a human IgG Fc variant, is new,
XX INDEPENDENT CLAIMS are also included for the following: a Chinese hamster
XX ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in
XX its growth medium in excess of 10 microg per million cells in a 24 hour
XX period; and a method for making a recombinant fusion protein comprising
XX HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred
XX protein: The peptide linker containing 20 or fewer amino acids is present
XX between HuEPO and the human IgG Fc variant, and comprises two or more
XX amino acids selected from glycine, serine, alanine, and threonine. The
XX human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human
XX IgG2 with Pro31Ser mutation comprising 436 amino acids (SEQ ID NO. 18).
XX It also comprises a hinge, CH2, and CH3 domains of human IgG4 with
XX Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.
XX 20). It further comprises a hinge, CH2, and CH3 domains of human IgG1
XX with Leu234Val, Leu235Ala, and Pro31Ser mutations comprising 435 amino
XX acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro
XX biological activity similar to or higher than that of rHuEPO on a molar
XX basis. Preferred CHO-derived cell line: The CHO-derived cell line
XX producing the HuEPO-L-vFc fusion protein in its growth medium in excess
XX of 30 microg per million cells in a 24 hour period. The human IgG Fc
XX variant comprises a hinge, CH2, CH3 domains of human IgG selected from
XX IgG1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,
XX the IgG Fc contains amino acid mutations to attenuate effector functions,
XX a flexible peptide linker containing 20 or fewer amino acids is present
XX between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion
XX protein exhibits in vitro biological activity similar to or higher than
XX that of rHuEPO on a molar basis. Preferred Method: Making a recombinant
XX fusion protein comprising HuEPO, a flexible peptide linker, and a human
XX IgG Fc variant comprising: generating a CHO-derived cell line; growing the
XX cell line where the recombinant protein is expressed in its growth medium
XX in excess of 10 microg per million cells in a 24 hour period; and

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 17, 2006, 08:33:21 ; Search time 21.2844 Seconds
(without alignments)
1966.430 Million cell updates/sec

Title: US-10-761-593A-22

Perfect score: 2312
Sequence: 1 MGHECPAMWLILSLSLP.....MHKALNNHTOKSLSPGK 435

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1217	52.6	255	4	S31866
2	1217	52.6	330	1	GHRU
3	1211	52.4	374	2	S69339
4	1164	50.3	234	2	PT0207
5	1141.5	49.4	326	1	G2HU
6	1134	49.0	327	1	G4HU
7	1130	48.9	377	2	A23511
8	1128	48.8	377	2	A60764
9	1105	47.8	289	1	G3HWT
10	994	43.0	193	1	ZHUH
11	902.5	33.0	192	1	U00173
12	902.5	33.0	328	2	I47160
13	902.5	33.0	328	2	I47159
14	901.5	33.0	323	1	GHRB
15	897.5	38.8	192	1	I84613
16	897	38.8	277	2	I47162
17	887.5	38.4	328	2	I47158
18	886	38.3	329	1	G2GP
19	878.5	38.0	328	2	I47161
20	871.5	37.7	470	2	S22080
21	839	36.3	472	2	S31459
22	837	36.2	308	2	C30554
23	833.5	36.1	329	1	G3MSC
24	829.5	35.9	333	2	PS0018
25	824.5	35.7	444	2	PC4436
26	822.5	35.6	398	1	G3MSM
27	815.5	35.3	326	2	PS0017
28	814.5	35.2	324	1	G1MS
29	809.5	35.0	393	1	G1MSM

30	802	34.7	469	2	S37483	Ig gamma-2a chain
31	797.5	34.5	188	1	I46083	erythropoietin pre
32	796.5	34.5	329	2	S00847	Ig gamma-2c chain
33	793	34.3	330	1	G2MSA	Ig gamma-2a chain
34	788	34.1	339	1	G2MSM	Ig gamma-2a chain
35	786	34.0	335	1	G2MSAB	Ig gamma-2a chain
36	782.5	33.8	322	2	PS0019	Ig gamma-2a chain
37	778	33.7	446	2	S40295	Ig gamma-2a chain
38	777.5	33.6	474	1	G2MS11	Ig gamma-2b chain
39	771.5	33.4	192	1	S28148	erythropoietin pre
40	771.5	33.4	327	2	S06611	Ig gamma-2 chain C
41	765.5	33.1	194	1	I46401	erythropoietin pre
42	765	33.1	405	1	G2MSBM	Ig gamma-2b chain
43	761.5	32.9	190	2	I46578	erythropoietin - p
44	751.5	32.5	192	1	A24902	erythropoietin pre
45	751	32.5	475	2	S01321	Ig gamma-2b chain

ALIGNMENTS

RESULT 1

S31866
Ig gamma-1 chain C region - synthetic

C/Species: synthetic

A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

Query Match

Best Local Similarity 98.7%; Pred. No. 1.9e-75; Length 255;

Matches 224; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	209	DKHTCPCPAPBPAVAGSPVFLPPPKDITLMSRPPEVTCVVDVSHEDPEKFNMYVD	268
DB	29	DKHTCPCPAPBPAVAGSPVFLPPPKDITLMSRPPEVTCVVDVSHEDPEKFNMYVD	88
QY	269	GVEVHNAKTPREBOVNSTYRVSVLTVLHQMNGEKYCKVSNKALPASIETISKAK	328
DB	89	GVEVHNAKTPREBOVNSTYRVSVLTVLHQMNGEKYCKVSNKALPAPIETISKAK	148
QY	329	GQPREPVYTLPSRDELITNOVSLTCLVKGFPSPDIIVWESNGCPENNYKTPPTLDS	388
DB	149	GQPREPVYTLPSRDELITNOVSLTCLVKGFPSPDIIVWESNGCPENNYKTPPTLDS	208
QY	389	DGSEFLYSKLTVDKSRWQGNVSCSVMEHAIHNNHTOKSLSPGK	435
DB	209	DGSEFLYSKLTVDKSRWQGNVSCSVMEHAIHNNHTOKSLSPGK	255

RESULT 2

GHRU
Ig gamma-1 chain C region - human

C/Species: Homo sapiens (man)

A:Residues: 1-330 <ELL>
A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370
A>Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A>Note: Lys-330 is removed after translation
R:Harrie, L.J
Submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: UNIPARC:UPI0000133CFE; EMBL:Z17370
R:Yakubashin, N.; Ueda, S.; Odate, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A>Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:681139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113,235-330 <TAK>
A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A>Title: The covalent structure of a human gammag-immunoglobulin. VI. Amino acid sequence
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96,'R','98-135 <CUN>
A:Cross-references: UNIPARC:UPI000017378D
A>Note: This sequence has the G1m(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A>Title: The covalent structure of a human gammag-immunoglobulin. VIII. Amino acid sequence
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-151,'Q','156-165,'Q','167-176,'Q','178-194,'N','196-197,'D','199-238,'E','240,
A:Cross-references: UNIPARC:UPI000017378E
A>Note: This sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R:Ponslating, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physik. Chem. 357, 1571-1604, 1976
A>Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q','36-96,'K','98-115,'Q','117-197,'D','199-238,'D','240,'L','242-268,'E','272
A:Cross-references: UNIPARC:UPI000017378F
A>Note: This sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physik. Chem. 364, 713-747, 1983
A>Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289331; PMID:6884994
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R','98-197,'D','199-238,'E','240,'W','242-266,'D','268-271,'D','273-330 <SCH>
A:Cross-references: UNIPARC:UPI0000173790
A>Note: This sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A>Title: The covalent structure of a human gammag-immunoglobulin. X. Intrachain disulfide
A:Reference number: A90565; MUID:71064027; PMID:5923144
A:Contents: annotation; disulfide bonds
R:Decker, L.; Schwarz, U.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physik. Chem. 357, 1515-1540, 1976
A>Title: Rule of antibody structure, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
A:Genetics:
Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Intron: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
P:20-85/Domain: immunoglobulin homology <IM1>
P:137-206/Domain: immunoglobulin homology <IM2>
P:243-310/Domain: immunoglobulin homology <IM3>
P:27-83,144-204,250-308/Disulfide bonds: #status experimental
P:103/Disulfide bonds: interchain (to light chain) #status experimental
P:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
P:189/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 52.6%; Score 1217; DB 1; Length 330;
Best Local Similarity 98.7%; Pred. No. 2.6e-75;
Matches 224; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 209 DKHTTCCPAPEVAGSPSFLFPKPKDTLMSRPEVTCVVVDVSHEDPEVKFMYVD 268
104 DKHTTCCPAPELGGPSVFLFPPKPKDTLMISRPVTCVVVDVSHEDPEVKFMYVD 163
269 GVEVHNAKTPREQVNSTYRVVSVLTVTHQDMLNGEKYCKVSNALPAPISKEITISKAK 328
164 GVEVHNAKTPREQVNSTYRVVSVLTVTHQDMLNGEKYCKVSNALPAPISKEITISKAK 223
Dy 329 GQPREPQVYTLPPSRDELFTNVNYSLTCLVKGFYPSDIAVEMESNGOPENNYKTTTPVLDS 388
224 GQPREPQVYTLPPSRDELFTNVNYSLTCLVKGFYPSDIAVEMESNGOPENNYKTTTPVLDS 283
Dy 389 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPK 435
284 DGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPK 330

RESULT 3
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlich, A.A.; Auctourier, P.; Pred'homme, J.L.; Cogne, M.
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Accession number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X61695
R:Khamlich, A.A.
submitted to the EMBL Data Library, September 1994
A:Accession number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140; C'142-374 <KH2>
A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X61695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 52.4%; Score 1211; DB 2; Length 374;
Best Local Similarity 97.8%; Pred. No. 7.7e-75;
Matches 222; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Dy 209 DKHTTCCPAPEVAGSPSFLFPKPKDTLMSRPEVTCVVVDVSHEDPEVKFMYVD 268
148 DKHTTCCPAPELGGPSVFLFPPKPKDTLMISRPVTCVVVDVSHEDPEVKFMYVD 207
269 GVEVHNAKTPREQVNSTYRVVSVLTVTHQDMLNGEKYCKVSNALPAPISKEITISKAK 328
208 GVEVHNAKTPREQVNSTYRVVSVLTVTHQDMLNGEKYCKVSNALPAPISKEITISKAK 267

Gy	14	I S P P D A S A N P L T I T I A D F R K L I F R Y S F L -----R G U -K L Y T G E A C R F G D S G G G S G	199
D b	151	M T Q S P A S L S V S V G E L V T I T C R A S E N T Y S L A M Y O Q K O K S P Q L L V A A T N L A D G V P R F S	21.0
Gy	200	G G G S -----G G S -----D K H T C P C P	21.8
D b	211	G S S G S G Y S L K I N S L O S E D P G S Y Y C O H F M C T P Y T F G G G T R L E I K R S C D K H T C P G P	27.0
Gy	219	A P V A G A G S F L P P P K X D T I M S R P E T C V U D V S H E D P V K W Y V O S V E Y H A N K T	27.8
D b	271	A P E L D G S F L P P P P K O T I M S R P E T C V U D V S H E D P V K W Y V O S V E Y H A N K T	33.0
Gy	279	P R E Q V N S T R Y V S T Y L H O M L N K E K C V S K A L P A S E K T I S A K O P R E P V Y T	33.8
D b	331	P R E Q V N S T R Y V S V L V H O M L N K E K C V S K A L P A P L E K T I S A K O P R E P V Y T	39.0
Gy	339	L P P R D E L T N O V S L T C L Y K G F P S D I A V E S N Q P E N N Y K T T P P V L D S G S F L Y S K L	39.8
D b	391	L P P R D E L T N O V S L T C L Y K G F P S D I A V E S N Q P E N N Y K T T P P V L D S G S F L Y S K L	45.0
Gy	399	T V D K S R W O Q G N V F S C S V M E A L H N H T O K S I S L S P G K	43.5
D b	451	T V D K S R W O Q G N V F S C S V M E A L H N H T O K S I S L S P G K	48.7

RESULT 2			
06GMW7_HUMAN	PRELIMINARY;	PRT;	475 AA.
ID	OG6MW7		
AC	OG6MW7		
DT	05-JUL-2004	(TREMBLrel. 27, Created)	
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)	
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homindaes;		
OC	Homio.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Splice;		
RX	MEBLINL=22388257; PubMed=12477932; DOI=10.1073/pnas.942603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Ziegler B., Buetow K.H., Scheefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Dickenson L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stegleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udell T.B., Tothiyuki S., Carinini P., Prange C.,		
RA	Rana S.S., Loughnan N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bohak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.J., Huilyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faney J., Helton E., Keteeman M., Maden A.C., Rodrigues S., Sanchez A.,		
RA	Whiting M., Maden A., Young A.C., Shevchenko V., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield A., Schein J.E., Krzyzinski M.I., Skalska U.,		
RA	Schnecker A., Schein J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RL	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Splice;		
RL	Strausberg R.		
RL	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC073782; AA:73782.1; -; mRNA.		
DR	GO; GO:0016021; CA:integral to membrane; IEA.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG CL.		
DR	InterPro; IPR003506; IG MHC.		

Accession	Protein	Score	Length	Indels	Gaps
DR InterPro: IPR003596; Ig V.		52.78	1218.5	DB 2	475
DR Pfam: PF07654; C1-beet. 3.		64.28			
DR SMART: SM00409; IG: 2.					
DR SMART: SM00407; IGc1: 3.					
DR SMART: SM00406; IGV: 1.					
DR PROSITE: PS50835; IG_LIKE: 4.					
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.					
KM Hydrophobic Protein.					
SO SEQUENCE 475 AA; 51987 MW; 2A1FE5D736860F8 CRC64;					
Query Match		52.78	Score 1218.5	DB 2	Length 475;
Best Local Similarly		64.28	Pred. No. 1.6e-82;		
Matches 251; Conservative		27;	Mismatches 50;	Indels	63;
					Gaps 10;

Oy	7	DTEVNFYAMKREVEGQAVIEW--QG-LALLSEVALRGGL-----L	108
		:	
Dd	123	DTCLNTFY-----YGLDVGCGQTITIVISASIKGPSVFPPLAPSSKTSIGGTALGCL	173
		: : : : :	
Oy	109	YNSSQWPEPQLGHVDKA--VSLRSBLTLLIALAG--AKKELISPDDAASAAPRTIADT	164
Dd	174	VKQIFP-EEPTYSWMNGSALTSCVHTTFPAVLDSGLIXLSLVVPF--SSSLGTOTYICNV	230
Oy	165	FRLFLRVSNFNLRGKLKLYTGACRFTGDGGSGGSGGGSGGSDKTHTPPCPAPBVAQ	224
Dd	231	NHRFSNKTVD-----KKVERPSG-----DKHHTCPGPAPBILG	264
Oy	225	GSPVLPFPKPCKDTLMISRTPENTCVVDVSHEDPEVKNNYVDGEVHNATKPREEQY	284
Dd	265	GPSPVLPFPKPCKDTLMISRTPENTCVVDVSHEDPEVKNNYVDGEVHNATKPREEQY	324
Oy	285	NSTRYRVSVYLTVLHDQMNLGSKKYCKVCNSNKALPASIEKTTISKAKGPRBPVYTLPPSRD	344
Dd	325	NSTRYRVSVYLTVLHDQMNLGSKKYCKVCNSNKALPASIEKTTISKAKGPRBPVYTLPPSRD	384
Oy	345	ELTKNOVSILTCLVKGKGYPSPDIAVEMESNGQPENNYKTPPYLSDSGSFPLYSKLTVDKSR	404
Dd	385	ELTKNOVSILTCLVKGKGYPSPDIAVEMESNGQPENNYKTPPYLSDSGSFPLYSKLTVDKSR	444
Oy	405	MOOGANVFSGSVMEHALHHNHYTOKSLSLSPGK	435
Dd	445	MOOGANVFSGSVMEHALHHNHYTOKSLSLSPGK	475

RESULT 3

ID	IGHG1_HUMAN	STANDARD;	PRT;	330 AA.
1D	IGHG1_HUMAN			
AC	P01857;			
DC	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
CC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.U., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RU	Nucleic Acids Res. 10:4071-4079 (1982).			
RL	[2]			
RP	PROTEIN SEQUENCE OF I-115 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Wardak M.J., Belman G.M.;			
RU	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments HI-H4.";			
RN	Biochemistry 9:3161-3170(1970).			
RP	[3]			
RP	PROTEIN SEQUENCE OF I36-329 (EU).			

QY 301 WLNKGEYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGF 360
DB 301 WLNKGEYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGF 360
QY 361 YPSDIAVEMESNGOPENNYYKTTPEVLDSGSPFLYSKLTVDKSRMOOGNVFSCSVMEAL 420
DB 361 YPSDIAVEMESNGOPENNYYKTTPEVLDSGSPFLYSKLTVDKSRMOOGNVFSCSVMEAL 420
QY 421 HNHHTOKSLSLSPGK 435
DB 421 HNHHTOKSLSLSPGK 435

RESULT 2
US-09-932-812A-20
; Sequence 20, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: increased biological
; FILE REFERENCE: 02SUN2001
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuPO-L-vFc gamma4 with a 27-amino acid leader peptide
; OTHER INFORMATION: (Figure 2B
; OTHER INFORMATION:)
US-09-932-812A-20

Query Match 96.0%; Score 2220; DB 2; Length 437;

Best Local Similarity 95.7%; Pred. No. 3.5e-195;

Matches 418; Conservative 10; Mismatches 7; Indels 2; Gaps 1;

QY 1 MGVECPAWMLMLLSLPLGLPVIGAPPRILICDSRVLERYLLEAKEENITTCGAHC 60
DB 1 MGVECPAWMLMLLSLPLGLPVIGAPPRILICDSRVLERYLLEAKEENITTCGAHC 60
QY 61 SLNENITVPDTKVFYAMKMEVGOAVVEWOGIALISEAVLRGOALLVNSSQPWEPLQ 120
DB 61 SLNENITVPDTKVFYAMKMEVGOAVVEWOGIALISEAVLRGOALLVNSSQPWEPLQ 120
QY 121 HVKAVSGLSLTLTLRALGAQKEAISPPDAASAARITTTADTFRLKFRVYSNFLRGKL 180
DB 121 HVKAVSGLSLTLTLRALGAQKEAISPPDAASAARITTTADTFRLKFRVYSNFLRGKL 180
QY 181 KLVTEGACRTGDSGGSGSGSGSGSGSGSDKTH--TCPPCAPAEVAGSPVFLPPPKKDT 238
DB 181 KLVTEGACRTGDSGGSGSGSGSGSGSGSDKTH--TCPPCAPAEVAGSPVFLPPPKKDT 238
QY 239 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTRPREOYNSTRVVSVLTVLH 298
DB 239 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTRPREOYNSTRVVSVLTVLH 298
QY 241 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTRPREOYNSTRVVSVLTVLH 300
DB 241 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTRPREOYNSTRVVSVLTVLH 300
QY 299 QDMLNGEKYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 358
DB 299 QDMLNGEKYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 358
QY 301 QDMLNGEKYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 360
DB 301 QDMLNGEKYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 360
QY 359 GFYPSDIAVEMESNGOPENNYYKTTPEVLDSGSPFLYSKLTVDKSRMOOGNVFSCSVME 418
DB 359 GFYPSDIAVEMESNGOPENNYYKTTPEVLDSGSPFLYSKLTVDKSRMOOGNVFSCSVME 418
QY 361 GFYPSDIAVEMESNGOPENNYYKTTPEVLDSGSPFLYSKLTVDKSRMOOGNVFSCSVME 420
DB 361 GFYPSDIAVEMESNGOPENNYYKTTPEVLDSGSPFLYSKLTVDKSRMOOGNVFSCSVME 420
QY 419 ALHNHTOKSLSLSPGK 435
DB 419 ALHNHTOKSLSLSPGK 435

DB 421 ALHNHTOKSLSLSPGK 437

RESULT 3
US-09-932-812A-18
; Sequence 18, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: increased biological
; FILE REFERENCE: 02SUN2001
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HuPO-L-vFc gamma2 with a 27-amino acid leader peptide
; OTHER INFORMATION: (Figure 2
; OTHER INFORMATION: A)
US-09-932-812A-18

Query Match 95.9%; Score 2216.5; DB 2; Length 436;

Best Local Similarity 95.9%; Pred. No. 7.3e-195;

Matches 419; Conservative 9; Mismatches 6; Indels 3; Gaps 2;

QY 1 MGVECPAWMLMLLSLPLGLPVIGAPPRILICDSRVLERYLLEAKEENITTCGAHC 60
DB 1 MGVECPAWMLMLLSLPLGLPVIGAPPRILICDSRVLERYLLEAKEENITTCGAHC 60
QY 61 SLNENITVPDTKVFYAMKMEVGOAVVEWOGIALISEAVLRGOALLVNSSQPWEPLQ 120
DB 61 SLNENITVPDTKVFYAMKMEVGOAVVEWOGIALISEAVLRGOALLVNSSQPWEPLQ 120
QY 121 HVKAVSGLSLTLTLRALGAQKEAISPPDAASAARITTTADTFRLKFRVYSNFLRGKL 180
DB 121 HVKAVSGLSLTLTLRALGAQKEAISPPDAASAARITTTADTFRLKFRVYSNFLRGKL 180
QY 181 KLVTEGACRTGDSGGSGSGSGSGSGSGSDK--THTCPAPAEVAGSPVFLPPPKKDT 238
DB 181 KLVTEGACRTGDSGGSGSGSGSGSGSGSDK--THTCPAPAEVAGSPVFLPPPKKDT 238
QY 239 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTRPREOYNSTRVVSVLTVLH 298
DB 239 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTRPREOYNSTRVVSVLTVLH 298
QY 240 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTRPREOYNSTRVVSVLTVLH 299
DB 240 LMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTRPREOYNSTRVVSVLTVLH 299
QY 299 QDMLNGEKYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 358
DB 299 QDMLNGEKYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 358
QY 300 QDMLNGEKYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 359
DB 300 QDMLNGEKYKCKVSNKALPASIEKTISSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVK 359
QY 359 GFYPSDIAVEMESNGOPENNYYKTTPEVLDSGSPFLYSKLTVDKSRMOOGNVFSCSVME 418
DB 359 GFYPSDIAVEMESNGOPENNYYKTTPEVLDSGSPFLYSKLTVDKSRMOOGNVFSCSVME 418
QY 419 ALHNHTOKSLSLSPGK 435
DB 419 ALHNHTOKSLSLSPGK 435
QY 420 ALHNHTOKSLSLSPGK 436
DB 420 ALHNHTOKSLSLSPGK 436

RESULT 4

US-09-968-362A-22

; Sequence 22, Application US/09968362A

; Patent No. 6797493

; GENERAL INFORMATION:

; APPLICANT: Sun, Lee-Hwei K

; APPLICANT: Sun, Bill

GenCore version 5.1.7
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OM protein - protein search, using BW model

Run on: April 17, 2006, 08:40:49 ; Search time 62.8555 Seconds
(without alignments)
2891.644 Million cell updates/sec

Title: US-10-761-593a-22

Sequence: 1 MGVECPAMWMLLSLSLP.....KHEALHNYTKSLSPGK 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2312	100.0	435	3 US-09-932-812-22	Sequence 22, Appl
2	2312	100.0	435	4 US-10-761-593a-22	Sequence 22, Appl
3	2312	100.0	435	6 US-11-016-518a-22	Sequence 22, Appl
4	2312	100.0	435	6 US-11-017-185-22	Sequence 22, Appl
5	2220	96.0	437	3 US-09-932-812-20	Sequence 20, Appl
6	2220	96.0	437	4 US-10-761-593a-20	Sequence 20, Appl
7	2220	96.0	437	6 US-11-016-518a-20	Sequence 20, Appl
8	2220	96.0	437	6 US-11-017-185-20	Sequence 20, Appl
9	2216.5	95.9	436	3 US-09-932-812-18	Sequence 18, Appl
10	2216.5	95.9	436	4 US-10-761-593a-18	Sequence 18, Appl
11	2216.5	95.9	436	6 US-11-016-518a-18	Sequence 18, Appl
12	2216.5	95.9	436	6 US-11-017-185-18	Sequence 18, Appl
13	2197.5	95.0	428	4 US-10-435-608-10	Sequence 10, Appl
14	2197.5	95.0	428	4 US-10-622-108-10	Sequence 10, Appl
15	2197.5	95.0	428	5 US-10-841-250-24	Sequence 24, Appl
16	2048	88.6	425	4 US-10-435-608-8	Sequence 8, Appl
17	2048	88.6	425	4 US-10-622-108-8	Sequence 8, Appl
18	1983.5	85.8	444	5 US-10-841-250-16	Sequence 16, Appl
19	1337.5	57.9	447	3 US-09-968-362-22	Sequence 22, Appl
20	1337.5	57.9	447	5 US-10-800-497-22	Sequence 22, Appl
21	1337.5	57.9	447	5 US-10-800-449-22	Sequence 22, Appl
22	1308.5	56.6	430	5 US-10-841-250-22	Sequence 22, Appl
23	1307	56.5	358	6 US-11-045-022-2	Sequence 2, Appl
24	1297.5	56.1	377	6 US-11-045-022-4	Sequence 4, Appl
25	1281	55.4	294	4 US-10-433-108-26	Sequence 26, Appl
26	1281	55.4	302	4 US-10-433-108-25	Sequence 25, Appl
27	1276	55.2	287	4 US-10-433-108-23	Sequence 23, Appl

28	1276	55.2	287	4 US-10-433-108-28	Sequence 28, Appl
29	1276	55.2	287	4 US-10-433-108-31	Sequence 31, Appl
30	1268.5	54.9	269	4 US-10-609-217-10	Sequence 10, Appl
31	1268.5	54.9	269	4 US-10-632-388-10	Sequence 10, Appl
32	1268.5	54.9	269	4 US-10-651-723-10	Sequence 10, Appl
33	1268.5	54.9	269	4 US-10-645-761-10	Sequence 10, Appl
34	1268.5	54.9	269	4 US-10-666-696-10	Sequence 10, Appl
35	1268.5	54.9	269	4 US-10-653-048-10	Sequence 10, Appl
36	1268.5	54.9	269	5 US-10-645-784-10	Sequence 10, Appl
37	1265.5	54.7	277	4 US-10-609-217-20	Sequence 20, Appl
38	1265.5	54.7	277	4 US-10-632-388-20	Sequence 20, Appl
39	1265.5	54.7	277	4 US-10-651-723-20	Sequence 20, Appl
40	1265.5	54.7	277	4 US-10-645-761-20	Sequence 20, Appl
41	1265.5	54.7	277	4 US-10-666-696-20	Sequence 20, Appl
42	1265.5	54.7	277	4 US-10-653-048-20	Sequence 20, Appl
43	1265.5	54.7	277	5 US-10-645-784-20	Sequence 20, Appl
44	1265	54.7	347	4 US-10-272-899a-108	Sequence 108, Appl
45	1264	54.7	250	4 US-10-609-217-1070	Sequence 1070, Ap

ALIGNMENTS

RESULT 1
US-09-932-812-22
; Sequence 22, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biologic
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HUBO-L-vfc gammal with a 27-amino acid leader peptide (figure 2
US-09-932-812-22

Query Match	Score	DB 3:	Length	435:
Best Local Similarity	100.0%	Pred. No. 2e-153;		
Matches	435;	Conservative	0;	Mismatches
0;			Indels	0;
0;			Gaps	0;
QY	1	MGVECPAMWMLLSLSLPGLPVLGAPPRILCDSEVLERVLLFAKEAENITTGCAEHC	60	
DB	1	MGVECPAMWMLLSLSLPGLPVLGAPPRILCDSEVLERVLLFAKEAENITTGCAEHC	60	
QY	61	SLNENITVPTKVFYAMKREVGQAWEVQGLALISEAVLRGQALLVNSQPMPELQL	120	
DB	61	SLNENITVPTKVFYAMKREVGQAWEVQGLALISEAVLRGQALLVNSQPMPELQL	120	
QY	121	HYDKAVSGRSITTLIRALGAQKEAISPDAASAALRTITDTPFKLFRVYNSPFRGKL	180	
DB	121	HYDKAVSGRSITTLIRALGAQKEAISPDAASAALRTITDTPFKLFRVYNSPFRGKL	180	
QY	181	KLYTGACRTGDSGGSGGSGGSGGSDKTHCPCPAPAEVAGSPVFLFPKPKDTLM	240	
DB	181	KLYTGACRTGDSGGSGGSGGSGGSDKTHCPCPAPAEVAGSPVFLFPKPKDTLM	240	
QY	241	ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKRREQYNSTRVSVLTIVLHOD	300	
DB	241	ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKRREQYNSTRVSVLTIVLHOD	300	
QY	301	WLNKGYKCKVSKKALPASIEKTISSAKGQPRPPQVYTLTPSPSDELTKQOVSLTCLVKGF	360	
DB	301	WLNKGYKCKVSKKALPASIEKTISSAKGQPRPPQVYTLTPSPSDELTKQOVSLTCLVKGF	360	

QY 361 YPSDIAVEMESNGOPENNYKTTTPVLDSDGSFPLYSKLTVDKSRMOQGNVFSQVWHEAL 420
DB 361 YPSDIAVEMESNGOPENNYKTTTPVLDSDGSFPLYSKLTVDKSRMOQGNVFSQVWHEAL 420
QY 421 HNHYYTQKSLSLSPGK 435
DB 421 HNHYYTQKSLSLSPGK 435

RESULT 2
US-10-761-593A-22
; Sequence 22, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HUEPO-L-vfc gamma1 with a 27-amino acid leader peptide (Figure
; US-10-761-593A-22

Query Match 100.0%; Score 2312; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 2e-153;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGVHECPAMWLLLSLSPGLPVLGAPPRILICDSRVLERLYLEAKAEENITTCABHC 60
QY 61 SLNENITVPDTKVNPFYAMKMEVGOQAVEWOGIALISEAVLRGQALLVNSSQPMPELQI 120
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DB 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDAASAAPLRTITADTFPKLFRVYSNPLRGKL 180
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DB 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVLPFPKXDTLM 240
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DB 241 ISRTPEVTCTVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEOYNSTYRVSVLTCLVHOD 300
QY 301 WINGKEYKCKVSNKALPASIEKTIISAKGQPREPOVYTLPPSRDELITKNOVSLTCLVKGF 360
DB 301 WINGKEYKCKVSNKALPASIEKTIISAKGQPREPOVYTLPPSRDELITKNOVSLTCLVKGF 360
QY 361 YPSDIAVEMESNGOPENNYKTTTPVLDSDGSFPLYSKLTVDKSRMOQGNVFSQVWHEAL 420
DB 361 YPSDIAVEMESNGOPENNYKTTTPVLDSDGSFPLYSKLTVDKSRMOQGNVFSQVWHEAL 420
QY 421 HNHYYTQKSLSLSPGK 435
DB 421 HNHYYTQKSLSLSPGK 435

RESULT 3

US-11-016-518A-22
; Sequence 22, Application US/11016518A
; Publication No. US20050124045A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased
; FILE REFERENCE: 02SUN2004D1
; CURRENT APPLICATION NUMBER: US/11/016,518A
; CURRENT FILING DATE: 2004-12-17
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HUEPO-L-vfc gamma1 with a 27-amino acid leader peptide (Figure
; US-11-016-518A-22

Query Match 100.0%; Score 2312; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2e-153;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGVHECPAMWLLLSLSPGLPVLGAPPRILICDSRVLERLYLEAKAEENITTCABHC 60
QY 61 SLNENITVPDTKVNPFYAMKMEVGOQAVEWOGIALISEAVLRGQALLVNSSQPMPELQI 120
DB 61 SLNENITVPDTKVNPFYAMKMEVGOQAVEWOGIALISEAVLRGQALLVNSSQPMPELQI 120
QY 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDAASAAPLRTITADTFPKLFRVYSNPLRGKL 180
DB 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDAASAAPLRTITADTFPKLFRVYSNPLRGKL 180
QY 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDAASAAPLRTITADTFPKLFRVYSNPLRGKL 180
DB 121 HYDKAVSGRLSTLTLLRALGQKEAISPPDAASAAPLRTITADTFPKLFRVYSNPLRGKL 180
QY 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVLPFPKXDTLM 240
DB 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVLPFPKXDTLM 240
QY 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVLPFPKXDTLM 240
DB 181 KLYTGACRTGDSGGSGSGSGSDKTHTCPCPAPEVAGSPVLPFPKXDTLM 240
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DB 241 ISRTPEVTCTVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEOYNSTYRVSVLTCLVHOD 300
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DB 301 WINGKEYKCKVSNKALPASIEKTIISAKGQPREPOVYTLPPSRDELITKNOVSLTCLVKGF 360
QY 361 YPSDIAVEMESNGOPENNYKTTTPVLDSDGSFPLYSKLTVDKSRMOQGNVFSQVWHEAL 420
DB 361 YPSDIAVEMESNGOPENNYKTTTPVLDSDGSFPLYSKLTVDKSRMOQGNVFSQVWHEAL 420
QY 421 HNHYYTQKSLSLSPGK 435
DB 421 HNHYYTQKSLSLSPGK 435

RESULT 4
US-11-017-185-22
; Sequence 22, Application US/11017185
; Publication No. US20050142642A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological
; FILE REFERENCE: 02SUN2001D2

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OM protein - protein search, using sw model

Run on: April 17, 2006, 08:42:04 ; Search time 41.9037 Seconds

(without alignments)
441.079 Million cell updates/sec

Title: US-10-761-593A-22

Perfect score: 1 MGVECPAMLMILLISLSP...MEALHNYTKSLSPCK 435

Sequence: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
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2: /SIDSS/ptocdata/1/pubppa/US07_NEW_PUB pep: *
3: /SIDSS/ptocdata/1/pubppa/US07_NEW_PUB pep: *
4: /SIDSS/ptocdata/1/pubppa/PCT_NEW_PUB pep: *
5: /SIDSS/ptocdata/1/pubppa/US09_NEW_PUB pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197.5	95.0	428	US-11-029-003-24	Sequence 24, Appl
2	1983.5	85.8	444	US-11-029-003-16	Sequence 16, Appl
3	1308.5	56.6	430	US-11-029-003-22	Sequence 22, Appl
4	1268.5	54.9	281	US-10-841-956A-7	Sequence 7, Appl
5	1263.5	54.6	484	US-11-274-910-30	Sequence 30, Appl
6	1255.5	54.3	708	US-11-150-533-65	Sequence 65, Appl
7	1241	53.7	255	US-11-057-923-5	Sequence 5, Appl
8	1241	53.7	515	US-10-954-468-33	Sequence 33, Appl
9	1241	53.7	516	US-10-954-468-32	Sequence 32, Appl
10	1241	53.7	518	US-10-954-468-31	Sequence 31, Appl
11	1241	53.7	519	US-10-954-468-30	Sequence 30, Appl
12	1238	53.5	386	US-11-075-047A-58	Sequence 58, Appl
13	1237	53.4	459	US-10-949-720-390	Sequence 390, Appl
14	1235.5	53.4	476	US-11-274-910-23	Sequence 23, Appl
15	1233	53.3	320	US-11-183-205-50	Sequence 50, Appl
16	1230.5	53.2	303	US-11-087-719-71	Sequence 71, Appl
17	1229	53.2	270	US-10-841-956A-5	Sequence 5, Appl
18	1229	53.2	489	US-10-835-475-11	Sequence 11, Appl
19	1229	53.2	514	US-10-835-475-2	Sequence 2, Appl
20	1228.5	53.1	467	US-11-075-047A-40	Sequence 40, Appl
21	1227	53.1	404	US-10-948-053-7	Sequence 7, Appl
22	1226.5	53.0	469	US-11-075-047A-38	Sequence 38, Appl
23	1226	53.0	321	US-11-186-422-8	Sequence 8, Appl
24	1225	53.0	696	US-11-029-003-8	Sequence 8, Appl
25	1224.5	53.0	352	US-11-075-047A-34	Sequence 34, Appl

26	1224.5	53.0	452	US-11-016-503-6	Sequence 6, Appl
27	1224.5	53.0	455	US-11-016-503-14	Sequence 14, Appl
28	1224.5	53.0	455	US-11-089-803-4	Sequence 4, Appl
29	1224.5	53.0	455	US-11-218-234-4	Sequence 4, Appl
30	1224.5	53.0	455	US-11-204-709-10	Sequence 10, Appl
31	1224	52.9	423	US-11-029-003-10	Sequence 10, Appl
32	1224	52.9	464	US-11-075-047A-42	Sequence 42, Appl
33	1223.5	52.9	473	US-11-075-047A-36	Sequence 36, Appl
34	1223	52.9	292	US-11-087-719-73	Sequence 73, Appl
35	1223	52.9	292	US-11-087-719-75	Sequence 75, Appl
36	1223	52.9	370	US-11-075-047A-18	Sequence 18, Appl
37	1223	52.9	455	US-11-075-047A-32	Sequence 32, Appl
38	1223	52.9	467	US-11-197-488-25	Sequence 25, Appl
39	1223	52.9	480	US-11-075-047A-48	Sequence 48, Appl
40	1223	52.9	492	US-11-197-488-27	Sequence 27, Appl
41	1223	52.9	572	US-11-075-047A-44	Sequence 44, Appl
42	1222.5	52.9	462	US-11-016-503-8	Sequence 8, Appl
43	1221.5	52.8	375	US-11-075-047A-54	Sequence 54, Appl
44	1221.5	52.8	557	US-11-016-503-4	Sequence 4, Appl
45	1221	52.8	251	US-11-242-294-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-11-029-003-24
Sequence 24, Application US/11029003
Publication No. US20050260194A1
GENERAL INFORMATION:
APPLICANT: PETERS, ROBERT T.
APPLICANT: MEZO, ADAM R.
APPLICANT: RIVERA, DANIEL S.
APPLICANT: BITONTE, ALAN J.
APPLICANT: STATTEL, JAMES
TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
FILE REFERENCE: 08945.0007-01000
CURRENT APPLICATION NUMBER: US/11/029,003
CURRENT FILING DATE: 2005-01-05
PRIOR APPLICATION NUMBER: 60/539,207
PRIOR FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: 60/487,964
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/469,600
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 24
LENGTH: 428
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-029-003-24
Query Match 95.0%; Score 2197.5; DB 7; Length 428;
Best Local Similarity 95.9%; Pred. No. 2.9e-167;
Matches 417; Conservative 2; Mismatches 9; Indels 7; Gaps 1;
QY 1 MGVECPAMLMILLISLSP...PLVGVGAPRLICDSRVLEKKAENITTCAGHC 60
DB 1 MGVECPAMLMILLISLSP...PLVGVGAPRLICDSRVLEKKAENITTCAGHC 60
QY 61 SLNENITVPTKYNFYAMKMEVGGQAVYVWQGLALISEAVLFGQALLVNSSQPWEPLQ 120
DB 61 SLNENITVPTKYNFYAMKMEVGGQAVYVWQGLALISEAVLFGQALLVNSSQPWEPLQ 120
QY 121 HVDKAVSGRLSTTLRLAIGAKQKASPPDAASAPLRTTADTPFKLFRVYGNFLRGL 180
DB 121 HVDKAVSGRLSTTLRLAIGAKQKASPPDAASAPLRTTADTPFKLFRVYGNFLRGL 180
QY 181 KLYTGACRTGDSGGGSGGGSGGSDKTHTCPPCAPAEVAGDSVFLPPKPKDTLM 240

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Db 181 KYTGACRGTGURE-----FAGAAAVKTHTCPCPCPAPBELLGGSGSVLPFPKPKDTLM 233
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Db 234 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKPREEQYNSTYRVSVLTJVLHOD 293
Qy 301 WLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGF 360
Db 294 WLNKGEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGF 353
Qy 361 YPSDIAVEMESNQCPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRWQOGNVFSCSVNHEAL 420
Db 354 YPSDIAVEMESNQCPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRWQOGNVFSCSVNHEAL 413
Qy 421 HNNHYTKSLISPGK 435
Db 414 HNNHYTKSLISPGK 428
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RESULT 2

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US-11-029-003-16
; Sequence 16, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEN, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029, 003
; PRIOR FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539, 207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487, 964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469, 600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-11-029-003-16
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Query Match 85.8%; Score 1983.5; DB 7; Length 444;
Best Local Similarity 85.2%; Pred. No. 3.2e-150;
Matches 390; Conservative 3; Mismatches 20; Indels 45; Gaps 3;
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Qy 66 ITTPDKRVNRYAKRMKREVGQAVWOGALLSEAVIRGOALLVNSQPEPQLAVDKA 125
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Qy 218 PAEVAGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKT 277
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Db 227 PABELLGGSGSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKT 286
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Qy 338 TLPPSRDELTKNQVSLTCLVKGFPSDIAVEMESNQCPENNYKTTTPVLDSDGSFPLYSK 397
Db 347 TLPPSRDELTKNQVSLTCLVKGFPSDIAVEMESNQCPENNYKTTTPVLDSDGSFPLYSK 406
Qy 398 LTVDKSRWQOGNVFSCSVNHEALHNNHYTKSLISPGK 435
Db 407 LTVDKSRWQOGNVFSCSVNHEALHNNHYTKSLISPGK 444
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RESULT 3

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US-11-029-003-22
; Sequence 22, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEN, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029, 003
; PRIOR FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539, 207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487, 964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469, 600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-11-029-003-22
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Query Match 56.6%; Score 1308.5; DB 7; Length 430;
Best Local Similarity 63.9%; Pred. No. 1.6e-96;
Matches 265; Conservative 26; Mismatches 57; Indels 67; Gaps 5;
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Qy 100 AVLRGOALLVNSQPEPQLAVDKAVSGLRSLITLLRALGAKENISPPDAASAPLRT 159
Db 121 CVIQG-----VGVTETPIMEDSILAV----- 142
Qy 160 ITADTFRKLFRVYSNLRGK-----LKYTGACRGTGDSGGSGG 200
Db 143 -----RKYFQRIITLYLKEKTKYSPCAMEVYRAIMRMSFSLTNLQESLASKG-GGGSGG 195
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Db 196 GSGGGSGSKTHTCPCPCPAPAEVAGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPE 255
Qy 261 VKNMYVVDGVEVNAKTKPREEQYNSTYRVSVLTJVLHODWLNKGEYKCKVSNKALPAPI 320
Db 256 VKNMYVVDGVEVNAKTKPREEQYNSTYRVSVLTJVLHODWLNKGEYKCKVSNKALPAPI 315
Qy 321 EKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEMESNQCPENNYK 380
Db 316 EKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEMESNQCPENNYK 375
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